

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 19, 2002, 07:52:31 : Search time 1919 Seconds
(without alignments)
4994.452 Million cell updates/sec

Title: US-09-807-459-2
Perfect score: 2359
Sequence: 1 MAPSDVGDVTKTLAASES.....DPKALIRKVSLEADNLLER 458

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DOCALLIGN=200 -THR_SCORE=Pct -THR_MAX=100 -ALIGN=40 -MODE=LOCAL
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-TGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
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32: em_hgt_other:*
33: em_hgtgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	2359	100.0	1810	3	AB017700
2	2355	99.8	1943	3	AF092736
3	996.5	42.2	1542	6	A16430
4	831.5	35.2	2089	3	AF030060
5	831.5	35.2	2306	3	AF030058
6	830.5	35.2	2223	3	AF030061
7	827.5	35.1	1962	3	BBO5BWER
8	827.5	35.1	1962	6	I12361
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10	826.5	35.0	1990	3	BBDONAC
11	826.5	35.0	2087	3	BBDONAC
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21	790	33.5	2005	3	BBDONAC
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23	770.5	32.7	2796	3	BBDONAC
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33	532	22.6	575	3	AF014762
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36	527	22.3	575	3	AF014767
37	520	22.0	574	3	AF014764
38	520	22.0	823	3	AF014759
39	513	21.7	575	3	AF014763
40	513	21.7	866	3	AF014765
41	476	20.2	670	3	AF092735
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43	442.5	18.8	1016	3	AF017297
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45	440.5	18.7	1016	3	AF017295

ALIGNMENTS

RESULT 1
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LOCUS AB017700 1810 bp mRNA linear INV 11-DEC-1999
DEFINITION Babesia caballi pBC48/31 mRNA for 48KDa merozoite antigen, complete cds.
ACCESSION AB017700
VERSION AB017700.1 GI:5821173
KEYWORDS 48KDa merozoite antigen; BC48/31.
SOURCE Babesia caballi (strain:USDA) CDNA to mRNA.

ORGANISM	REFERENCE	TITLE	JOURNAL	MEDLINE REFERENCE	AUTHORS	FEATURES
Babesia caballi	1 (sites)					
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;						
Babesia.						
Ikeda, H., Xuan, X., Igarashi, I., Tanaka, S., Kanemaru, T.,						
Nagasawa, H., Fujisaki, K., Suzuki, N. and Mikami, T.						
Cloning and expression of a 48-kilodalton babesia caballi merozoite						
rhoity protein and potential use of the recombinant antigen in an						
enzyme-linked immunosorbent assay						
J. Clin. Microbiol. 37 (11), 3475-3480 (1999)						
2 (bases 1 to 1810)						
Ikeda, H., Xuan, X., Igarashi, I., Tanaka, T., Abgandorjijn, A.,						
Inoue, N., Nagasawa, H., Fujisaki, K., Mikami, T., Toyoda, Y. and						
Suzuki, N.						
Direct Submission						
Submitted (16-SEP-1998) Hiroshi Ikeda, Obihiro University of						
Agriculture and Veterinary Medicine, The Research Center for						
Protozoan Molecular Immunology, Inadaoka Nishi 2 Sen 13, Obihiro,						
Hokkaido 080-8555, Japan (E-mail: d09013@obihiro.ac.jp,						
Tel: 81-155-49-5647, Fax: 81-155-49-5643)						
Location/Qualifiers						
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ORIGIN						
polyA-site						
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Query Match:	100.00%	Indels:	0			
Db:	3	Gaps:	0			
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Db	99	GTCGACGACGCTGCAATGCGCTATATATATCAACAGTCGCAATGAGGATTAATTCGGCT	158			
OY	41	ValSerAspAlaPheAlaGluArgLLeuGlySerSerGlnValProlyGlySerAsnGlySer	60			
Db	159	GTGCTGCACACTGCGCGAGCGCATTTGGACATGAGTCCCTAAGGGAGATTAATGAC	218			
OY	61	AlaSerValSerAlaTyrMetSerValGlyAlaLysGlnAspGlyLeuThrLeuGlnSer	80			
Db	219	GCTTCGCTTAAGCGCATATAGTGGCGGCTACACAGAGACTGGCTGATCTCCAAAGT	278			

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Db	279	CTTAAGTACCCTCTTGAGCGTAAGTACCAACCGCTGACCTTCTGACCCCTTACCACTTG	338
QY	101	GUUAaAaAaPheLLeuPheLysGlnSerAspAlaAsnProAlaAsnSerThrgLnLys	120
Db	339	GAGCGCCGATTTATACCTTCTCAAGAGAGGACGCTAAATCGGCCAAATGACACTGAGAAG	398
QY	121	ArgheTrpMetArgPheArgArgGlyLysAsnHisSerTyrThrHisAspLeuValPhe	140
Db	399	CGCTTCGATGCGCTTTCACAAGGGGCAAAACACAGTTACTTTCACAGACTTAAGCTTTC	458
QY	141	AsnLeuLeuGlnLysAsnValThrArgAspAlaAspAlaThrAspLLeuLysnPheAla	160
Db	459	AATTCGTCGGAGAGAACCGTACTCCGACGCGGATGCTACTGACTTGAAGAACTTTGGG	518
QY	161	SerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPhe	180
Db	519	TTCAGGTACCTGTACATGGCCAGCGCTTACTTACAAACGTAACGAAATGTGATGATTC	578
QY	181	GlyAlaSerPhePheAsnLysLeuSerPheThrThrglyLeuPheLysTrpGlyLLeys	200
Db	579	GGTCTAGCTTCCTTAAACAAGTGTCTTTCACATACGCGGTGTGTCGGGGGCAACAAG	638
QY	201	ArgAlaLeuLysGlnLLeuLeArgSerAsnLeuProLeuAspLLeuLysThrgLnHisSer	220
Db	639	AGGGCACTTAAGCAGATTAATTCGCTCTACCTCGCCCTTACATCGGACAGACACACAC	698
QY	221	ValSerArgLeuGlnHisLLeuSerSerTyrLysAspTyrMetAspThrGlnLLeuPro	240
Db	699	GTCAGTGGCTGCAGCACATTTACGAGCAGATTACAAAGATTACATGGAATCCGACGATTCCT	758
QY	241	AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr	260
Db	759	GCACTGGCCCAAGTTGGGAAGCGCTTCTCCCTATGCTAGTGGAGAGCGTGGCTGGCCAC	818
QY	261	ValAlaGlyTyrValAspThrProTPTyrLysLysTrpTyrMetLysLeuLysAsnPhe	280
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QY	281	MetValAsnArgValPheLeuProThrLysLysPhePheAsnLysGlnLLeuArgGluPro	300
Db	879	ATGCTGAACAGGGGTTCATTCCTACAAAGAAATCTTCAATAGCAAAATTCGTGAGCCT	938
QY	301	SerLysAlaLeuLysGlnLysValSerThrAspThrLysAspLeuPheGlnLysnLLe	320
Db	939	AGTAAGGCATTTAAAGAAAGAGGTCAACGCAACCAAGGATTTATTCCAGAAACAATAAT	998
QY	321	GlyGlnGlyThrValAspPhePheAsnLysGlnLLeArgAspProSerLysAlaLeuLys	340
Db	999	GCGCAGGCTACTGTGCACTTCTTCATTAAGAAATTCGTGACCTGTAAGCATTTAAAN	1058
QY	341	GlnLysValSerAsnAspAlaLysAspLeuPheGlnLysnLysLLeuGlnGlyThrVal	360
Db	1059	GAAGAAATGTCAACAGCGCCAAAGGATTTATTGGAACAAATAATTCGCGACGGTACTG	1118
QY	361	AspPheLLeuAsnGlnLLeuArgAspProSerLysAlaLeuLLeuLArgLysValSerThr	380
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QY	381	GlyValaGlnAspLeuPheGlnLysnLysLLeuGlnGlyThrValAspPheLLeuAsn	400
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QY	401	GluLLeuArgAspProSerLysAlaLeuLLeuArgLysValTyrThrgLnLaaAspLLeu	420
Db	1239	GAATTCGTGACCCCTAGTAAGCATTAATTAAGAAAGTGTACACCCGAGGCCGATGATTTA	1298
QY	421	PheGlnLysnLysLLeuGlyGlnGlyThrValAspPheLLeuAsnLysGlnLLeuArgAspPro	440
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RESULT 2
 AF092736 1943 bp mRNA linear INV 29-JUN-1999
 LOCUS AF092736

DEFINITION Babesia caballi clone X6 rhoptry-associated protein 1 (RAP-1) mRNA.
 ACCESSION AF092736
 VERSION AF092736.1 GI:5230731
 KEYWORDS
 SOURCE Babesia caballi.
 ORGANISM Babesia caballi.
 Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.

REFERENCE 1 (bases 1 to 1943)
 AUTHORS Kappmeyer,L.S., Perryman,L.E., Hines,S.A., Baszler,T.V., Katz,J.B., Hemmeyer,S.G. and Knowles,D.P.
 TITLE Detection of equine antibodies to babesia caballi by recombinant B. caballi rhoptry-associated protein 1 in a competitive-inhibition enzyme-linked immunosorbent assay
 JOURNAL J. Clin. Microbiol. 37 (7), 2285-2290 (1999)
 MEDLINE 99294770
 PUBMED 10364599

REFERENCE 2 (bases 1 to 1943)
 AUTHORS Kappmeyer,L.S. and Knowles,D.P.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-1998) Agricultural Research Service, US Department of Agriculture, 337 Busted Hall, Washington State University, Pullman, WA 99164-7030, USA

FEATURES
 source Location/Qualifiers
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 119..1585
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BASE COUNT 528 a 438 c 498 g 479 t
 ORIGIN

Alignment Scores:
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 Score: 2355.00 Matches: 457
 Percent Similarity: 99.78% Conservative: 0
 Best Local Similarity: 99.78% Mismatches: 1
 Query Match: 99.83% Indels: 0
 Gaps: 0

US-09-807-459-2 (1-458) x AF092736 (1-1943)

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 Oy 21 Valaspsersal1aalasna1lat1rmet1leas1nser1asps1et1ser1aspt1r1leu1ser1ala 40
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RESULT 3
LOCUS A16430 1542 bp DNA linear PAT 23-MAR-1994
DEFINITION (Lambda EMBL3 #5) genes 1-4 encoding 21B4/rhoptry homologues.
ACCESSION A16430
VERSION A16430.1 GI:511979
KEYWORDS
SOURCE Babesia ovis.
ORGANISM Babesia ovis.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.
REFERENCE 1 (bases 1 to 1542)
AUTHORS BABESIAL ANTIGENS
TITLE Patent: WO 9314204-A 8-22-JUL-1993;
JOURNAL Location/Qualifiers
FEATURES
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GEMFY"
BASE COUNT 455 a 366 c 343 g 378 t
ORIGIN
Alignment Scores:
Pred. No.: 1,13e-71 Length: 1542
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Score: 62.648 Conservative: 81
Best Local Similarity: 44.848 Mismatches: 153
Query Match: 42.248 Indels: 18
Gaps: 6
US-09-807-459-2 (1-458) x A16430 (1-1542)

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Oy 81 LeuLysTyrProLeuGlnAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeu 100
Db 331 GTCACATCACCCCGTGTGATGAGAAATACCAACCTTATCACTCCCAACCCCTACCAATGG 390
Oy 101 GGuilearAlaPheIleLeuPheLysGlnSerAspAlaAsnProAlaAsnSerThrGlyLys 120
Db 391 GATGCTGCTTCTACTTGTGTTCAAGAACTCTGCTGAAACCCGCTAAATAATGTTTAAA 450
Oy 121 ArgPheTyrMetArgPheArgArgLysAsnHisSerTyrPheHisAspLeuValPhe 140
Db 451 GGTCAATGGATCGCTTCCGAAACGGAAACAAATGAGTACACACCGTTCCTCATTT 510
Oy 141 AsnLeuLeuGlnLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAla 160
Db 511 GCTGTGTGGCAAAAGCGGTTACTGTGAGATGGTGTGCTGACTGACCTGTGATCTCTGCTGC 570
Oy 161 SerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPhe 180
Db 571 AACAGCCTTTTGTACATGGCCACACCTATTACAAACCTACTAATGTGTCAACAACAGC 630
Oy 181 GAlaAserPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrPolylLeuLys 200
Db 631 GATGCCAATCTTTTAAACGAGATGCTTCCGCAACAAAGATTTTGGTTTGGTATCAAG 690
Oy 201 ArgAlaLeuLysGlnIleIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSer 220
Db 691 AAGGCGCTCAAGAGATGCTGCTGCAATGTCTCCGAATATATGGA---GAGACAGT 747
Oy 221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIlePro 240
Db 748 ATGAAACCATTTAGCATTTTGGCCACGCTTACAAAGGACTACATGTTCACCAATTCACA 807
Oy 241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr 260
Db 808 ACCCTTCAAAATTTTCCGCAACGCTTACTGATGATGATGATGATGATGATGATGATGATG 867
Oy 261 ValAlaGlyTyrValAspThrProThrPheTyrLysTyrPheTyrMetLysLeuLysAsnHe 280
Db 868 CTCGCGGCTTATGATCAAGCTTCATGTCACAGATGATGATGATGATGATGATGATGATGAT 927
Oy 281 MetValAsnArgValPheIleProThrLysLysPhePheAsnLysGluIleArgGluPro 300
Db 928 TTTGTTAACAAATATGCAACACCTACAAAGAACCTTCACAAAC---AAACACCA 981
Oy 301 SerLysAla---LeuLysGlnLysValSerThrAspThrLysAspLeuPheGluAsnLys 319
Db 982 CGCACCGCGCAATTTTTCGACAAAGATGCATGCAACCGCACCAAGACTTCTTCGACAAAG 1041
Oy 320 IleGlyGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeu 339
Db 1042 ATAGTGTCTCCCTACCAAGACTTCTTTCGAAACAAGATAGTGTCTCTACCAAGACTTTC 1101
Oy 340 LysGlu---LysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGly 358
Db 1102 TTCGAGAACAGATAGTGTCTCTACCAAGACTTCTTCGAGAACAGATAGTGTCTCTCT 1161
Oy 359 ThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysVal 378
Db 1162 ACCAAGACTTCTTTCGAGAACAAAGATAGTGTCTCTACCAAA----- 1203
Oy 379 SerThrGlyAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIle 398
Db 1204 -----GACTTCTTTCAGAACAAAGATAGTGTCTCTCTACCAAGACTTCTTTC 1248
Oy 399 AsnAsnGluIleArgAspProSerLysAlaLeuIle---ArgLysValTyrThrGluAla 417
Db 1249 GAGAACAGTCTCCCTCAACGCAACAGACTTCTTCGAGAACAAAGCTGCTGCAACACAC 1308
Oy 418 AspAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnLysGluIle 437

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Db 1309 AAGCACTCTTCGAGAACACCTGCGTCAACACCAAGCACTTCTTGAGACACAGATT 1368
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Qy 438 Argasproserlysalaleuilearglyvalserthrghuala 452
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Db 1369 GGTGCCCCCATTAAGA-ATCATTTGAGACTGGACACAGCG 1412
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RESULT 4
AF030060
LOCUS AF030060 2089 bp DNA linear INV 13-NOV-1997
DEFINITION Babesia bovis strain ur rhoptry associated protein-1 (rap-1) gene,
complete cds.
ACCESSION AF030060
VERSION AF030060.1 GI:2613066
KEYWORDS
SOURCE Babesia bovis.
ORGANISM Babesia bovis.
          Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
          Babesia.
REFERENCE 1 (bases 1 to 2089)
AUTHORS Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
TITLE Structure, sequence, and transcriptional analysis of the Babesia
JOURNAL bovis rap-1 multigene locus
REFERENCE 2 (bases 1 to 2089)
AUTHORS Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
Washington State University, Pullman, WA 99164, USA
FEATURES
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       /strain="ur"
       /db_xref="taxon:5865"
       /note="Isolated in Uruguay"
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       /gene="rap-1"
       /note="gene copy 2"
       22..1719
       /gene="rap-1"
       /product="rhoptry associated protein-1"
       /protein_id="AAB84270.1"
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NHGDYHVFVGLNNVNHGEGTDVELVKLVYMATMNYKTLTVSMNAKFFNFR
SEFTKISRRIKOTLSDIRNMVDEDEFEERIERITOLTSYEDMLTOIPTLKSPAR
RYADMVKVLLGSLTSYVEAPWYKRWTKKRPDSKVTQPTKKRPIDNTNVTNLYK
ANVAEPTKKFMQDTHKTKGLAKENVAEPTKFFKEAPQVTKHFFDDNIGQPTFEFR
EAPQATNHFLENIGQPTKEFREAPQATNHFLENIAQPTKEFFKDVPOVTKRVITE
NIAQPTKEFREAPQATNHFLENIAQPAKTIIEFGGANFISAAHEGKQPLNTE
VGQPTKEFLNCALETTRDALHHLGKSSSEANPYDATENTQANDSTTNSGSDTAGYL"
BASE COUNT 659 a 447 c 411 g 572 t
ORIGIN

Alignment Scores:
Pred. No.: 3.59e-58 Length: 2089
Score: 831.50 Matches: 179
Percent Similarity: 51.70% Conservative: 80
Best Local Similarity: 35.73% Mismatches: 193
Query Match: 35.25% Indels: 49
Db: 3 Gaps: 6

US-09-807-459-2 (1-458) x AF030060 (1-2089)
Qy 1 MetlaprosaraspserValglyaspyalrhyrlystrhrleuLeualaalaSerluser 20
Db 112 CTCGCTCAGCTGAAGTGTAGTGATTTAACTCCACATTGGAACACAGCTATACTTGG 171
Qy 21 ValaspserAlaalaSerAlaalyrMetlleasnsSeraspmetSeraspTyrleuserAla 40
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Db 172 ATGACTCTCCGTGACACATGCACAACTTAAGATATGAACATGTTTGGACAAT 231
Qy 41 Valseraspasrphalaglunargilecysserghlnvalprolysglyserasnysser 60
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Db 232 GGTCTGTAGACAGATTGTAATGATGTCTTAACTGCTCCGAGACCTCCAACTGCTGT 291
Qy 61 AlaserValserAlatyrmeterargcysalalyglnaspCysleuthrleuglnser 80
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Db 292 GAGTAGTATTAACTATTATGCTGACCGTGTGAAATGACGATGCTTTACGATTGACAT 351
Qy 81 LeulysTyrProleuGlualalystrghlnProleuthrLeupProaspProtyrghlnleu 100
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Db 352 GTCAATATATCCGTTGTATCAACAGTACCAACCTATATCTTCCAAACCTTACAGTTG 411
Qy 101 GlualaalaPhelileuPhelysluseraspAlaasnProalaasnSerthrghluyys 120
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Qy 121 ArgphetrpmetarqPhearqargglyLysasnHisserTyrPheHisaspLeuValphe 140
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Db 472 CGCGAATGTTCCGTTTCAGAAATGAGAGAACCATGCGATTACACTTCCGCTCACT 531
Qy 141 AsnleuleuGlulysasnValthrargaspAlaaspAlaThrAspIleGlunspheala 160
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Db 532 GGTCTGTGACACAAATGTTGTGCACGAGAAAGAACTACCGATGTTGATATCTTGTGC 591
Qy 161 SerargTyrleuTyrmetAlaThrleuTyrTyrlystrThyTyrThrasnValaspLeuphe 180
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Db 592 AACCAAGTACTCTATATGCTATGACATGAACCTCAAGACTTATTGACAGCTAAACGTATG 651
Qy 181 GlyAlaserPhePheAsnLysleuserPheThrThrglyLeupheglYrplylelyys 200
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Db 652 AACGCCAGTTTCAACAGATTCAGCTTCACTACAAAGATTTAGTCGTGCTATTAAG 711
Qy 201 ArgAlaLeuLysghlnleleargserasnleuproleuasplleolythrghlnhisser 220
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Db 712 CAACATGAGTATGATATCATGAGTGAATGTTCTCGAAGATTTT---CAAGAAGAGAC 768
Qy 221 ValseratgleuGlnHislethrSerTyrLysAspTyrmetAspThrGlnleupro 240
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Db 769 ATCGAAGCTATCATCACTTACTGACAGCTACGAGATGATATGATGTGACCCAGATTCCA 828
Qy 241 AlaLeuProLysPheAlaLysArpPheSerLeuMetValaGlArgLeuLeuAlaThr 260
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Db 829 ACTCTTTCCAACTTTCACAGCTGCTTATGCTGACATGCTGAAGAAGTTTGTGCTCGTAC 888
Qy 261 ValAlaGlyTyrValAspThrProTyrTyrLysTyrTyrMetLysleuLysasnph 280
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Db 889 TTGACCTGCTAGCTTGAAGCTCCTTGTTGTAAGAAGATGATAAGAATTCAGAGACTTT 948
Qy 281 MetValasnArgValPheIleProThrLysLysPhe----- 292
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 949 TTCTGTAAAMAAGTTAACCCAACTTACAAAGAAGTTCATGAGAGATACTAACGAATTAC 1008
Qy 292 ----- 292
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Db 1009 AAAAACTATCTGAAMCCCAATGTTGCTGAGCCCACTAAAAAGTTTATGCGAGACACTAC 1068
Qy 293 -----PheasnLysgluIlearggluProserLysAlaLeuLysglu 306
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Db 1069 GAAAAAACCAAGGCTATGTAAGAGATGTAGCGCAACTTACACTTTTTCACAG 1128
Qy 307 LysValSerThrAspThrLysAspLeuPhegluasnLysIleGlyGlnGlyThrValasp 326
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Db 1129 GAGGCTCTCAAGTCAACCAACACTTCTCGATGATTAACATTGGCCCAACCCCAAGGAG 1188
Qy 327 PhePheasnLysgluIleargaspProserLysAlaLeuLysgluLysLysasnasp 346
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1189 TTTTTCAGGGAAGCTCCCAACCCCACTTAACATTTCCTAGACGAAAAAATTCGCTAACCA 1248
Qy 347 AlaLysaspLeuPhegluasnLysIleGlyGlnGlyThrValaspPheIleasnnglu 366
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Db 1249 ACCAAGAGATCTTC---ACGAGAGCTCTCTCAAGCACTAACCACTTCTTACAGCAAT 1305

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OY	367	11eAtgAapPProSeRerLyAlaLeuIleArGlySVaISetThnGIyAlaGlubAspleuThe	386
OY	367		
Db	1306	AATTGGTCAACCTACTACAAAGATTTTTCGAAGATGTCCCTCAAGTCACCAGAAGGTTATA	1365
OY	387	GUAAnLysILegLYInGLyThrValAspPhe-----	397
Db	1366	ACTGAGAACATTCGTCACMACCACTAAGAGATTCCTTAGAGAGTGCTCAGCTCACATG	1425
OY	398	----11eaSnAnGLuIleArGAsPProSerLySaLaLeuIleArGlySVaIThr	415
Db	1426	AAAGCTCTTAAGAAACAACATTGCCTCAACCTGCCAAGAAGAAATCATACAGAGTTGGTACA	1485
OY	416	GUAlaAsPaSPLeuPhLuAnsLySILegLYInGLyThrValAsPheLeuInslys	435
Db	1486	GGCGCCAGAGAT--TTCACTTCCCAGCCAGCCCATGAAGGACTACAGACGCTTTAAACGAA	1542
OY	436	GUlileArGaSPProSeRerLySaLaLeuIleArG--LysVaISerThGLuaLaSpAsn	454
Db	1543	ACTGTTGGCCAAACCTACAAAGGAATTCCTGAACGAGCTTTAGAAACATCAATAAACGCCA	1602
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Db	1603	TTA 1605	
RESULT 5			
LOCUS	AF030058	2306 bp DNA linear INV 13-NOV-1997	
DEFINITION	Babesia bovis strain CG-P rhoptry associated protein-1 (rap-1)		
ACCESSION	AF030058		
VERSION	AF030058.1		
KEYWORDS	GI:2613062		
SOURCE	Babesia bovis.		
ORGANISM	Babesia bovis		
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;		
AUTHORS	Babesia.		
TITLE	1 (bases 1 to 2306) Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F. Structure, sequence, and transcriptional analysis of the Babesia bovis rap-1 multigene locus		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 2306) Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-OCT-1997) Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164, USA		
FEATURES	Location/Qualifiers		
SOURCE	1..2306		
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BASE COUNT	756 c 475 k 438 g 636 t 1 others		

[illegible]

Db 1009 AAAAAATATGTGAAGCAATGTGTGAGCCACTAAAAAGTTATGACAGACTCAC 1068
Qy 293 -----PheasnlysgluilearggluProserlysalaleuylsngu 306
Db 1069 GAAAAAACCAAGCTATCTGAAAGAAATGTAGCCGAACCTACCTATTTTTCAG 1128
Qy 307 LysValSerThrAspThrIleuArgGluAspPheGluAsnlyslleGlyGlnGlyThrValAsp 326
Db 1129 GAGGCTCCCTCAAGTACCAACAACTCTTCGATGATTAACATTGGCCAAACCCACAGAG 1188
Qy 327 PhePheAsnLysGluIleArgAspProserLysAlaLeuLysGluLysValSerAsnAsp 346
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Qy 347 AlaLysAspLeuPheGluAsnlyslleGlyGlnGlyThrValAspPheIleAsnAsnGlu 366
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Db 1306 ATTGCTCAACCTACTTAACAAATTTTCAAGATGTCTCCCAAGTCAACCAAGAGTTATA 1365
Qy 387 GluAsnLysIleGlyGlnGlyThrValAspPhe----- 397
Db 1366 ACTGAGAACATGTGCTCAACCACTAAGAGATGCTTAGGAGGTTCTCATGCTACCATG 1425
Qy 398 -----IleAsnAsnGluIleArgAspProserLysAlaLeuIleArgLysValThr 415
Db 1426 AAGTCTTGAATGAAGAACTGTCTCAACCTGCCAAGAAATCATACATGTTGGTGA 1485
Qy 416 GluAlaAspAspLeuPheGluAsnlyslleGlyGlnGlyThrValAspPheIleAsnLys 435
Db 1486 GCGCCCAAGAAAT---TTCATTTCCGACGCCCATGAAGGACTTACGATTTCTTAACGAA 1542
Qy 436 GluIleArgAspProserLysAlaLeuIleArg---LysValSerThrGluAlaAspAsn 454
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Qy 455 Leu 455
Db 1603 TTA 1605
RESULT 6
AF030061 2323 bp DNA linear INV 13-NOV-1997
LOCUS Babesia strain ur rhoptry associated protein-1 (rap-1) gene,
DEFINITION complete cds.
ACCESSION AF030061
VERSION AF030061.1 GI:2613068
KEYWORDS
SOURCE Babesia bovis.
ORGANISM Babesia bovis.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.
REFERENCE 1 (bases 1 to 2323)
AUTHORS Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
TITLE Structure, sequence, and transcriptional analysis of the Babesia
bovis rap-1 multigene locus
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 2323)
TITLE Direct Submission
JOURNAL Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
Washington State University, Pullman, WA 99164, USA
FEATURES
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/db_xref="taxon:5865"
/note="Isolated in Uruguay"
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CDS
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BASE COUNT 745 a 485 c 454 g 637 t 2 others
ORIGIN
Alignment Scores:
Pred. No.: 4.91e-58 Length: 2323
Score: 830.50 Matches: 179
Percent Similarity: 51.70% Conservative: 80
Best Local Similarity: 35.73% Mismatches: 193
Query Match: 35.21% Indels: 49
DB: 3 Gaps: 6
US-09-807-459-2 (1-458) x AF030061 (1-2323)
Qy 1 MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSer 20
Db 164 CTGCTCCACAGCTAAAGTGTAGTGATTTAACTCCACATGGAACACGTGATCTTG 223
Qy 21 ValAspSerAlaAlaAsnAlaIleArgMetIleAsnSerAspMetSerAspThrLeuSerAla 40
Db 224 ATGACTCTCCGTGACCAACATGACACACATTAAGATGATGAACATGTTTGGACAA 283
Qy 41 ValSerAspAsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnGlySer 60
Db 284 GGTGCTGACACAGATTTGAATGATGTTGCTCAATGCTCTGAGACCTGCACTGCT 343
Qy 61 AlaSerValSerAlaIleArgMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer 80
Db 344 GAGCTAGTTAAACAATTATGCTGACCTGTGGAATGTAGCGATGCTTTACGATTGCAAT 403
Qy 81 LeuLysTyrlProLeuGluAlaLysTyrlProLeuThrLeuProAspProTyrlGlnLeu 100
Db 404 GTCAATATCCGTTGTATGCAAGAGTACCAACCTCTATCTTCCAAACCTTACCAAGTTG 463
Qy 101 GluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLys 120
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Qy 121 ArgPheThrPheLysPheArgArgGlyLysAsnHisSerTyrlPheHisAspLeuValPhe 140
Db 524 CCGGATGCTGTTGCTTCAACAAATGAGCAACCATGATTAACCATCTTCTGCTACT 583
Qy 141 AsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAla 160
Db 584 GGTCTGTTGCAACAATGTTGTGCACGAGAGAGAACTCCGATGTTGAATATCTGTGC 643
Qy 161 SerArgTyrlLeuTyrlMetAlaThrLeuTyrlTyrlTyrlThrAsnValAspGluPhe 180
Db 644 AACAAAGTACTATATGCTTACCAACTACAAACATTAATTGTACAGAGAAACACTATG 703
Qy 181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrlGlyLys 200
Db 704 AACGCCAAGTCTTCAACAGATTCACCTTACACAAAGATATATCAGTGTGCTATTAAG 763
Qy 201 ArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSer 220
Db 764 CAACATTTAGTATATCATCAGGTGAAATGTTCTCGAAGATTTT---GAAGAAAGAGAC 820


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Qy 221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetLaspThrGlnIlePro 240
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Db 821 ATCGACGATACACGACCTACTAGACGATACGACGATACGATACGATACGATACGATACG 880
Qy 241 AlaLeuPhePolysPheAlaLysArgPheSerLeuMetValValGlnArgLeuAlaThr 260
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Db 881 ACTGTTCCACAGATTTGACGCTGATATGCTGACATGCTGAGAAAGCTTCTGCTCGTAGC 940
Qy 261 ValAlaGlyTyrValAlaPheThrProTyrTyrLysLysTyrTyrMetLysLeuLysAsp 280
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Db 941 TTGACCTCTACGCTTGAAAGCTCTTGATCAAAAGATGATAGAAATTCAGAGACTTT 1000
Qy 281 MetValAsnArgValPheIleProThrLysLysPhe----- 292
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Db 1001 TTCCTAAAGAGTTACCAACCTACAAAGAGATTCATCGAGACTACGAGACTACGAGACT 1060
Qy 292 ----- 292
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Qy 293 ----- PheAsnLysGluIleArgGluProSerLysAlaLeuLysGlu 306
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Qy 307 LysValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAsp 326
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Qy 327 PhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsn 346
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Db 1241 TTTTTCAGGAAAGCTCCCAAGCCACTAAGATTTTCTTACGAAACATCGGTCACCA 1300
Qy 347 AlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGlu 366
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Qy 387 GluAsnLysIleGlyGlnGlyThrValAspPhe----- 397
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RESULT 7
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LOCUS         B. bigemina merozoite surface protein (p58) gene, complete cds.
ACCESSION     M60878
VERSION       M60878.1 GI:135860
KEYWORDS      merozoite surface protein.
SOURCE        Babesia bigemina merozoite DNA.
ORGANISM      Eukaryote; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
              Babesia.
REFERENCE     1 (bases 1 to 1662)

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AUTHORS      Mishra,V.S., Stephens,E.B., Dame,J.B., Perryman,L.E., McGuire,T.C.
              and McElwain,T.F.
TITLE        Immunogenicity and sequence analysis of recombinant p58: A
              neutralization sensitive, antigenically conserved Babesia bigemina
              merozoite surface protein
JOURNAL      Mol. Biochem. Parasitol. 47, 207-212 (1991)
MEDLINE      92049553
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    /db_xref="GI:155861"
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VSLIKRVVNDPESNDVENFASQIFYYTITLYKYRYLYLVDTPAKFKPLAFTPLBEF
GIQALKRILVRSNLPVDLGHPEATREIETISGTEIMTGYPAKTSFAERSKMATKT
LLTVSDSYVHLPAVKRMYRKFEIVNEFDPAKLIMKHVSQPKYATVLTLPENHO
AIRNVGOSTKRIANGVRLSRMIRESDQIIRKELPHYLISKAGAVENHVKKRSYV
PIKRGDPSAEAAVEETVPSGDSAEFEVEEEDQYDAVTVTQEVNSEKVDADAGNAE
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BASE COUNT   506 a      442 c      492 g      522 t
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Pred. NO.:    7e-58      Length:    1962
Score:        827.50     Matches:   181
Percent Similarity:  89.12%   Conservative: 75
Best Local Similarity: 41.80%   Mismatches: 140
Query Match:   35.08%     Indels:    37
                  Gaps:    12
us-09-807-459-2 (1-458) x BBOS8MER (1-1962)
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Qy 24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
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Db 624 ATGCGTTGAGAG-----AGCAGCCAGCGGACACATCACTTGTGTTAGCTTGTGG 677
Qy 144 GluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr 163
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Oy 164 LeuTYrMeLaIaThrLeuTYrLysThyTYrThrAsnValAspGluPheGlyAlaSer 183
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Oy 184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTYrGlyIleLysArgAlaLeu 203
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Db 858 AAGCGTTGGTTAGGAGCAACCTCCCGTTGACCTTGGAAC---CACCGTAGGCGCAC 914
Oy 224 LeuGlnHisIleThrSerSerTYrLysAspTYrMetLysAspThrGlnIleProAlaLeuPro 243
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Db 915 ATCCCGGAATATGCTAGCGGCTACGCGGAGTACATGATGACCAAGGCTGCGATGACC 974
Oy 244 LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGly 263
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 975 TCGTTCGGTGAAGCGTTTCCAAAGATGGCTACTAAGACTCTGTGGTTACCGTACAGCAG 1034
Oy 264 TYrValAspThrProTYrTYrLysLysTYrTYrMetLysLeuLysAsnPheMetValAsn 283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1035 TACGTCATTTGCCCGCGTACAGAGGTGGTACAGAACTTCAGAAATTCATTGTGAAC 1094
Oy 284 ArgValPheIleProThrLysLysPheAsnLysGluIleArgGluProSerLys--- 302
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Oy 375 IleArgLysValSerThrGlyLysGluAspLeuPheGluAsnLysIleGlyGlnGlyThr 394
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Db 1371 ---CAAAAGGGCGACCAACCATCCGAAAGCAGCTGTAGAGAAACCGTTCGCTGGC--- 1424
Oy 395 ValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValTYr 414
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Oy 415 Thr-----GluAlaAspAsp 419
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RESULT 8
LOCUS 112361 1962 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 1 from patent US 5422428.
ACCESSION 112361
VERSION 112361.1 GI:910384
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 (bases 1 to 1962)
TITLE Mcuire,T.C., McElvaine,T.F., Perryman,L.E. and Davis,W.C.
JOURNAL Immunization against babesiosis using purified surface antigens of
FEATURES Babesia bigemina and similar immunogens
Patent: US 5422428-A 1 06-JUN-1995;
Location/Qualifiers

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source 1..1962
BASE COUNT 506 a 442 c 492 g 522 t
ORIGIN
Alignment Scores:
Pred. No.: 7e-58 Length: 1962
Score: 827.50 Matches: 181
Percent Similarity: 59.12% Conservative: 75
Best Local Similarity: 41.80% Mismatches: 140
Query Match: 35.08% Indels: 37
DB: Gaps: 12
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Oy 4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaIleSerGluSerValAspSer 23
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Oy 124 MetArgPheArgArgGlyLysAsnHisSerTYrPheHisAspLeuValPheAsnLeuLeu 143
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Oy 144 GluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTYr 163
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Oy 915 ATCCCGGAATATGACTAGCGGCTACGCGGAGTACATGATGACCCAGAGTGCCTCGATGACC 974
Oy 244 LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGly 263
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Qy 323 GLyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGIuLys 342
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Dh 1266 -----CCTAGCCAAACAATATTTCGTGAGAGCTGCTCTACTACTCTTTCTAAGCA 1316
Qy 357 GlnGlyThrValAspPheIleAsnAsnGluIleArgAsp-----ProSerLysAlaLeu 374
Dh 1317 AAGGAGCGCTTGAGCAGCAGCTGTAAAGAGTTAAATCCGTGTCCTGCAATAAG----- 1370
Qy 375 IleArgLysValSerThrGlyAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThr 394
Dh 1371 ---CAAAAGGCGCAGCAACCATCCAGACAGCTGTAGAGAAACCGTCCGTGCG--- 1424
Qy 395 ValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValTyr 414
Dh 1425 ---GATTTCGCGGAAACTGAAATTGTGAGCTCCCTGAAAGCAATACGTGATGCTTTACT 1481
Qy 415 Thr-----GluAlaAspAsp 419
Dh 1482 ACTCAGAGGTTTAAACAGGAGAGGTTGATGCCGACGAT 1520
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ACCESSION M85186
VERSION M85186.1 GI:155879
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SOURCE Babesia bigemina (strain Mexico) merozoite DNA.
ORGANISM Babesia bigemina
Eukaryota; Alveolata; Apicomplexa; Phloplasmida; Babesiidae;
Babesia.
REFERENCE 1 (bases 1 to 1962)
AUTHORS Mishra,V.S., McIwain,T.F., Dame,J.B. and Stephens,E.B.
TITLE Isolation, sequence and differential expression of the p58 gene
JOURNAL Mol. Biochem. Parasitol. 53, 149-158 (1992)
MEDLINE 92365724
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BASE COUNT 505 a 442 c 493 g 522 t
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Pred. No.: 8,43e-58 Length: 1962
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Percent Similarity: 58.89% Conservative: 74
Best Local Similarity: 41.80% Mismatches: 141
Query Match: 35.04% Indels: 37
Dh: 3 Gaps: 12
US-09-807-459-2 (1-458) x BBODNAC (1-1962)
Qy 4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaIleSerGluSerValAspSer 23
Dh 282 GCAAGAGGTGTTGAGATGTCTCCAGACCTTGCTGAAAGCAATGAGTGTCTCATCT 341
Qy 24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
Dh 342 GAATGTGAAGTACTCAGCTCAGCAAGATATGCAAACTCAATTGTCTTAATGTAAGAG 401

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Qy 84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAla 103
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Dh 678 AAGAAAGATGTGTAGCGGACCTGAATCAATGATGTGAGAACTGCGCATCGCATAC 737
Qy 164 LeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSer 183
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Qy 184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrPglyIleLysArgAlaLeu 203
Dh 798 TTCTTCAACAAAGCTTCTTCAACCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 857
Qy 204 LysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGlnHisSerValSerArg 223
Dh 858 AAGCGTTGTGAGGAGAACCTTCCGCTGACCTTGAAC---CACCTGAGGCCACC 914
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Dh 915 ATCCGCAAAATAGCAGGCGGCTGACGCGATGATGATGATGATGATGATGATGATGATG 974
Qy 244 LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGly 263
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Dh 1035 TACGTCATTTTGGCCCGCTACAGAGGTGTACAGAAAGTTCAAGAAATTCATTTGTGAC 1094
Qy 284 ArgValPheIleProThrLysLysPhePheAsnLysGluIleArgLysProSerLys--- 302
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Qy 343 ValSerAsnAspAlaLysAspLeuPheGluAsnLysIle-----Gly 356
Dh 1266 -----CCTAGCCAAACAATATTTCGTGAGAGCTGCTCTACTACTCTTTCTAAGCA 1316
Qy 357 GlnGlyThrValAspPheIleAsnAsnGluIleArgAsp-----ProSerLysAlaLeu 374
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DEFINITION	Babesia bovis 60 kda merozoite surface protein mRNA, complete cds.		
ACCESSION	M38218		
VERSION	M38218.1	GI:155883	
KEYWORDS	merozoite surface protein Bv60.		
SOURCE	B. bovis (strain Mo7) blood stage, CDNA to mRNA, clone pbv60.		
ORGANISM	Babesia bovis		
	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;		
REFERENCE	1 (bases 1 to 1990)		
AUTHORS	Suarez,C.E., Palmer,G.H., Jasmer,D.P., Hines,S.A., Perryman,L.E. and McElwain,T.F.		
TITLE	Characterization of the gene encoding a 60-kilodalton Babesia bovis merozoite protein with conserved and surface exposed epitopes		
JOURNAL	Mol. Biochem. Parasitol. 46 (1), 45-52 (1991)		
MEDLINE	91304520		
COMMENT	Direct entry and computer-readable sequence for [unpublished (1990)] kindly submitted by T.F.McElwain. 30-AUG-1990.		
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gene			
CDS			
BASE COUNT	628 a 437 c 398 g 527 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	8.58e-58	Length:	1990
Score:	826.50	Matches:	178
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Best Local Similarity:	35.53%	Mismatches:	195
Query Match:	35.04%	Indels:	49
DB:	3	Gaps:	6
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Dd	272	ATGACTCCGCGTGCACCATGCAACAACATTACTAAGAATGAATAAACATCTTTGGACAT	331
Oy	41	ValseraspasnPhaelagiuaArglieCyserGelvalProlysgLysersnysSer	60
Dd	332	GCTGCTGAGCAGATTGTAATAATGATGTTTGCTCTAATGCTCTGAGAGACTCCAACTGCT	391
Oy	61	AlaserValSerAlatarytmetSerasrcyalalysglinspcylsLeuthreungIne	80
Dd	392	GAGTAGTAAACATTTATGTCTGACCGTGGAAATGTACGAGTGCCTTACGATTGACAAT	451
Oy	81	LeutysyrProleunglualalysryrGlnProlethrLeuProaspprotyrctIne	100
Dd	452	GTCAAATATCCGGTGTATCAAGAGTACCAACCTATATCTTTCAAACCTTACCAAGTGG	511
Oy	101	GlualaIaPheilleLeuphelysgluserAspAlaasProalasnserthrcLulus	120
Dd	512	GATGCTCGGTTCAAGATTTGTTCAAAAGAGTGCATGACCCGTGCCAAGAACGCGTAA	571
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Oy	161	SerArgryleutyrmelatalarhleutyrrLystrTyrrThrasnValasplubhe	180
Dd	692	AACAGAGTACTCTATATGCGTACCATGACATCAAAAGCTTATTTGACATAAACAGATAG	751
Oy	181	GLYLaserPhebasnLulsleuserPhefthrcLyleuphedylyrpolylylys	200
Dd	752	AACGCCAAGTCTTCAACAAGATTCAGCTTACTACAAAGATTTACTGCTGCTATTAAG	811
Oy	201	ArgAlaleuLysglinlleleiarSerasnLeuproLeuasplleolyThrgluHisser	220
Dd	812	CAAACTTGAAGTATCATCATCAGAGTGAATGTTCTGGAAGATTTT---CAAGAAAGAGAC	868
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Dd	869	ATPCACACTATCACCTCAACTTACTAGACGCTACGAAGATTAATCTGTGCCACGATTTCCA	928
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Dd	929	ACTCTTCCAAAGTTTGACCGTCGTTATGCGCAATGTGAAGAAGTTTCTGCTCGTAGC	988
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Dd	1109	AAAAATATCTGAAGGCATGTTGCTGCGACCCACATAAAAAGTTTATGCAAGACACTCAC	1168
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Dd	1229	GAGGCTCTCAAGTACCAACAACACTTCTTGATGAGAACATTTGGCCAAACCCCAAGAG	1288
Oy	327	PhepheaenLysglulIeargasprProSerLysAlaleuLysglulLysValiserasnsp	346
Dd	1289	TTTTTTCAGGGAAGCTCCCAAGCACTAAACATTTCTAGACGAAGAAACCTCGGTCAACA	1348

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Db 1069 GAAAAAACCAAGGCTATCTGAAAGAGATGATGCGGCAACTACTTAAGACTTTTTCAG 1128
Qy 307 LysValSerThrAspThrLysAspLeuPheGluSnlylIleGlyInglYThrValAsp 326
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RESULT 12
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AF030053
LOCUS Babesia bovis strain S2P rhoptry associated protein-1 (rap-1) gene,
DEFINITION complete cds.
ACCESSION AF030053
AF030053.1 GI:2613052
VERSION
KEYWORDS
SOURCE
ORGANISM Babesia bovis.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.
REFERENCE
AUTHORS 1 (bases 1 to 2089)
TITLE Stutzer,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
STRUCTURE, sequence, and transcriptional analysis of the Babesia
bovis rap-1 multigene locus
JOURNAL Unpublished
2 (bases 1 to 2089)
AUTHORS Stutzer,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
Washington State University, Pullman, WA 99164, USA
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BASE COUNT 659 a 445 c 412 g 573 t
ORIGIN

Alignment Scores:
Pred. No.: 9,1e-58 Length: 2089
Score: 826.50 Matches: 178
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Best Local Similarity: 35.53% Mismatches: 195
Query Match: 35.04% Gaps: 49
DB: 3 Indels: 6

US-09-807-459-2 (1-458) x AF030053 (1-2089)

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Oy 398 -----IleAsnAsnGluLeileArgAspProSerLysAlaLeuLeileArgLysVal 415
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DEFINITION complete cds.
ACCESSION AF030055
VERSION AF030055.1 GI:2613056
KEYWORDS
SOURCE Babesia bovis.
ORGANISM Babesia bovis.
REFERENCE 1 (bases 1 to 2089)
AUTHORS Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
TITLE Structure, sequence, and transcriptional analysis of the Babesia
JOURNAL bovis rap-1 multigene locus
REFERENCE 2 (bases 1 to 2089)
AUTHORS Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
Washington State University, Pullman, WA 99164, USA

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source location/Qualifiers
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BASE COUNT 657 a 447 c 414 g 571 t
ORIGIN

Alignment Scores:
Pred. No.: 9,1e-58 Length: 2089
Score: 826.50 Matches: 178
Percent Similarity: 51.30% Conservative: 79
Best Local Similarity: 35.53% Mismatches: 195
Query Match: 35.04% Indels: 49
DB: 3 Gaps: 6

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Query Match:	35.04%
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Matches:	178
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Mismatches:	195
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US-09-807-459-2 (1-458) x AF030059 (1-2325)

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Db	232	GTCGTGTGACGAGATTGTAATATGATGTTGGCTCTAATGCTCTCGAGGACTCCACCTGCGT	291
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Db	292	GAGGAGATTAACTAATTTATGCTGACCGCTTGTAATGTACAGATGCTTTACGATTGACAAAT	351
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Db	352	GTCAAATATTCGGTTGTATCAAGATACCACCTCTACTCTCTCCAAACCCCTTACCAAGTTG	411
Oy	101	GluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLys	120
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Oy	241	AlaLeuProLysPheMetAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr	260
Db	829	ACTCTTTCCAAAGTTTGACAGCTGTATGCTACATGGGTGAAGAAAGGTTCTGCTCGTAGC	888
Oy	261	ValAlaGlyTyrValAspThrProTyrTyrLysLysTyrTyrMetLysLeuLysAspPhe	280
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Oy	281	MetValAsnArgValPheIleProThrLysLysPhe-----	292
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QY	307	LysValSerThrAspPthrLysAspLeuPhegluAsnlylIleglyInglyThrValAsp	326
Db	1129	GAGGCTCCTCAAGTACCAACAACACTTCTTCATGTAGAACATGTGGCAACCAACCAAGAG	1188
QY	327	PhePheasnlysgluileargysproserlysalaileuylsgluLysValSerAsnAsp	346
Db	1189	TTTTTTCAGGAGAGCTCCCAACCCACTAACAATTTCTTACAGAAACATCGGTCACCA	1248
QY	347	AlaLysAspLeuPhegluAsnlylIleglyInglyThrValAspPheIleasnnglu	366
Db	1249	ACCAAGAGACTTCTC---AGGAGGCTCTCTCAGCCACTAAGCACTTCTTACGAGAGAT	1305
QY	367	IleArgAspProSerLysAlaLeuIleArgLysValSerThrGlyAlaGluAspLeuPhe	386
Db	1306	ATTGCTCAACCTACTAAGAAGATTTTTCAGAGATGTCCCTCAAGTACCAAGAGAGTTATA	1365
QY	387	GluAsnlylIleglyInglyThrValAspPhe-----	397
Db	1366	ACTGAGAACATGTGCTCAACCACTAAGAGATGCTTACGAGAGTCTCATGCTACCATC	1425
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QY	416	GluAlaAspAspLeuPhegluAsnlylIleglyInglyThrValAspPheIleasnlyls	435
Db	1486	GCGCGCCAGAAAT---TTCATTTCCCGACGCCACTGAGAGTACTAAGCACTGTTAAACGAA	1542
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LOCUS	AF030056		
DEFINITION	Babesia bovis strain szp rhoptry associated protein-1 (rap-1) gene,		
ACCESSION	AF030056		
VERSION	AF030056.1	GI:2613058	
KEYWORDS			
SOURCE	Babesia bovis.		
ORGANISM	Babesia bovis		
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;		
AUTHORS	Babesia.		
TITLE	1 (bases 1 to 2385)		
JOURNAL	Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.		
REFERENCE	Structure, sequence, and transcriptional analysis of the Babesia		
AUTHORS	bovis rap-1 multigene locus		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 2385)		
REFERENCE	Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.		
AUTHORS	Direct Submission		
TITLE	Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,		
JOURNAL	Washington State University, Pullman, WA 99164, USA		
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				ANVAEPTRKFLQDTHETKGTGLKENVAEPTTFREARQVTRKFPDENTQTKFEFF
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				NIAPQTKFLREVEVTHAKVLNENIAQPAKEIIEFGTGARNFISAAHEGTQFLNEE
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BASE COUNT	772 a	492 c	465 g	655 t
OTHERS				1 others
Alignment Scores:				
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Score:	826.50	Matches:	178	
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Best local Similarity:	35.53%	Mismatches:	195	
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OY	21	ValASpSerAlaAlaAsnAlaTyrMetIleAsnSerASpMetSerASpTyrLeuSerAla	40	
DB	237	ATGACTCTCCGTCAGACATGCACATGCACAACATTACTAGAGATATGAACATGTTTGGACCAT	296	
OY	41	ValSerASpAsnPhaLeuGluArgLysIleCysSerGlnValProLysClySerAsnCysSer	60	
DB	297	GCTCGTCAGACAGATTGTAATGATGATTTGCTGCTTAATGCTCTGAGGAGCTCAACTGTCGT	356	
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DB	357	GAGGTAGTTAAACAATTATGCTGACGCGTGTGTAATGTACGGATGCTTATGCATTGCACAT	416	
OY	81	LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeu	100	
DB	417	GTCAAATATCCGTTTATCAACAGATACCAACCTCATCTTCACAAACCTTACCAAGTTG	476	
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DB	477	GATGCTGCGTTACAGATTGTTCAAAAGACATGCATGCMAACCTGCCAAGAACGCTGMAAA	536	
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DB	717	AACGCAAGTCTTCTCAACAGATTCAGCTACATCAAAAGATATTCAGTCGTCGATTAGG	776	
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LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE
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LOCUS	Babesia bovis phosphomannomutase homolog (pmn), rhotry associated protein-1 (rap-1) allele 1, rhotry associated protein-1 (rap-1) allele 2, and DnaJ homolog genes, complete cds.	AF027149	AF027149.1	GI:2731569	Babesia bovis.
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Qy	241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuAlaThr	260			
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Qy	261 ValAlaGlyTryValAspThrProTryLysLysTryPtryMetLysLeuLysAspPhe	280			
Db	954 TTGACCTCGTATCGATGGAAGCTCTTGGTACAAAGATGATAAAGAAATTGACAGACTTT	1013			
Qy	281 MetValAsnAlaGValPheIleProThrLysLysPhe-----	292			
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Qy	292 -----	292			
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Qy	387 GluAsnLysIleGlyGlnGlyThrValAspPhe-----	397			
Db	1431 ACTGAGACATTTGTCACCAACCTAAGAGAGTTCTTACGAGAGTTCTCATGCTACCATG	1490			
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Db	1491 AAAGCTTGAATGAACAACTTGTCTCAACCTCCCAAGGAATCATATCATGATGTTGGTACA	1550			
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ORGANISM Babesia bovis
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.
REFERENCE 1 (bases 1 to 1184)
AUTHORS Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
TITLE Structure, sequence, and transcriptional analysis of the Babesia
bovis rap-1 multigene locus
JOURNAL Mol. Biochem. Parasitol. 93 (2), 215-224 (1998)
MEDLINE 98327208
REFERENCE 2 (bases 1 to 1184)
AUTHORS Suarez,C.E., Palmer,G.H. and McElwain,T.F.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-1997) Veterinary Microbiology and Pathology,
Washington State University, Pullman, WA 99164-7040, USA
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Best Local Similarity: 35.538 Mismatches: 195
Query Match: 35.048 Indels: 49
DB: 3 Gaps: 6
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 VERSION AF030062.1 GI:2613070
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 Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
 Babesia.
 REFERENCE
 1 (bases 1 to 2325)
 Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
 Structure, sequence, and transcriptional analysis of the Babesia
 bovis rap-1 multigene locus
 Unpublished
 2 (bases 1 to 2325)
 Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
 Direct Submission
 Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
 Washington State University, Pullman, WA 99164, USA
 JOURNAL
 TITLE
 AUTHORS
 TITILE
 REFERENCE
 1. 2325
 Location/Qualifiers
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 /strain="R1A"
 /db_xref="taxon:5865"
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 BASE COUNT 766 a 477 c 437 g 642 t 3 others
 ORIGIN
 Alignment Scores:
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 Best Local Similarity: 36.53% Mismatches: 192
 Query Match: 34.99% Indels: 49
 DB: 3 Gaps: 8
 US-09-807-459-2 (1-458) x AF030062 (1-2325)

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Oy	21	ValAspSerAlaAlaAsnAla1aTyrMet1LeuSerAspMetSerAspTyrLeuSerAla	40
Db	172	ATGACTCCCGTGAACACATGCACACATTACTTAAGATATGAACAACATGTTTACGCAAT	231
Oy	41	ValSerAspAsnPhenAlaGluArg1LeuSerGlnValPro1ySglySerAsnCySer	60
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Db	292	GAGTAGTTAAACAATTAATAGCTGACCGCTTGTAATATGACGACTCTTACGATTGACAAAT	351
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Db	352	GTCAAATATCCGTTGTATCAAGATACCAACCTTATCTCTCCAAACCTTACCACTTG	411
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Db	412	GATGCTGGCTTCAACATTGTTCAAGAGAGTGCATCCAACTCCTGTAAGAACAGCGCTAAA	471
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Oy	201	ArgAlaLeu1ySgln1Le1ArgSerAsnLeuProLeuAsp1LeuGln1n1Ser	220
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Oy	221	ValSerArgLeuGlnHis1LeThrSerSerTyr1ySAspTyrMetAspThrGln1LePro	240
Db	769	ATCGAAGCTATCACTCAACACTTACTAGACGCTACGACAGATTTACATGTTGACCCACATTTCA	828
Oy	241	AlaLeuPro1ySPhenAla1ySArgPheSerLeuMetVal1yAlGlnArgLeuLeuAlaThr	260
Db	829	ACTCTTCCAAAGTTTGGCAGCTCGTATGCTACATGCTGGAAGAAGTTCGTCGCTGAC	888
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Oy	304	-----Leu1ySgln1ySValSerThrAspThr1ySAspLeuPheGlu	317
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QY	367	lleArgaspProSerLysAlaLeuIleArgLysValSerThrGlyAlaGluAspLeuPhe	386
DB	1306	ATTGCTCAACCTACTAAAGAAATTTTTCAGGGATGTCCTCAAGTCACCAAGAAAGGTATATA	1365
QY	387	GluAsnLysIleGlyGlnGlyThrValaspPhe-----	397
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DB	1426	AAAGCTTGTAATGAAACAAATGCTCAACCTGCGCAAGAAATCATATCAGATGGTGTACT	1485
QY	416	GluAlaAspAspLeuPheGluAsnLysIleGlyGlnGlyThrValaspPheIleAsnLys	435
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QY	436	GluIleArgaspProSerLysAlaLeuIleArg--LysValSerThrGluAlaAspAsn	454
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DB	1603	TTA 1605	
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KEYWORDS			
SOURCE	Babesia bigemina (strain Mexico) merozoite DNA.		
ORGANISM	Babesia bigemina		
	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;		
REFERENCE	1 (bases 1 to 2005)		
AUTHORS	Mishra,V.S., McElwain,T.F., Dame,J.B. and Stephens,E.B.		
TITLE	Isolation, sequence and differential expression of the p58 gene family of Babesia bigemina		
JOURNAL	Mol. Biochem. Parasitol. 53, 149-158 (1992)		
MEDLINE	92365724		
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QY	24	AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp	43

D	342	GAATGAGACAACTCAGTCAGTCACMAAGATATGCCAAAGTCATATGTTAAAGG	401
O	4	AsnPhelAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal	63
D	402	ACCATATGTTGGTGGATGGCTCGCAAGAAAGTTGTCGAAACACTACCTGCGGTGAGAGCTA	461
O	64	SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuTyr	83
D	462	ATTTGCTATGTGTTAAACCTTTGATGAGAGGCGATGTCTGACGCTTGACAGCATG-----	515
O	84	ProLeuGlnAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGlnAla	103
D	516	-----AGTACMAACCGCTTGACGTCTGCCAAATCTTACCAAGTTGGACGCTGCC	563
O	104	PhelIleLeuPheLysGlnSerAspAlaAsnProAlaAsnSerThrGlnLysArgPheTrp	123
D	564	TTTCATCGTTTTCACAGGAAGATGATTTAAACCTTCGCAAGAATGAGTGAAGCGCTTCTGG	623
O	124	MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeu	143
D	634	ATGCGTTCGAGG-----ACAGCGACAGGCGGACCTACCATCATTGTTGAGCTTGGTG	677
O	144	GluLysAsnValThrArgAspAlaAspAlaThrAspIleGlnLysAsnPhelAserArgTyr	163
D	678	AAGAAGAAATGTTTACCGCAGACCCGGAATCCAAATGATGTTGAGAACTTCCCATTCGCAATTC	737
O	164	LeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGlnubHegLysAser	183
D	738	TTTTCACATGACTACGTTGCTACTACAAAGCTTACCTGACGTTGACTTTACGGCGCTTAAG	797
O	184	PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrGlyLysArgLysArgLysLeu	203
D	798	TTCTTCACAAAGCTTGCTTTCACAACTCGCCTTTCGATTCGGTATCCAGAAAGCGTTG	857
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D	858	AAGCGTTGGTTAGAGACCAACTCCCGGTGACCTTGGAAAC---CACCTGAGGCCAC	914
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D	975	TCGTTCCGTGCGCTTCTCCAGATGGCTACTAACACTCTGTTGGTTACCGTCAGCGAC	1034
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D	1035	TACGCGCATTTGCCCGGGGTACAGAGGTGTTACAGAAATTCAGAGATTCATTTGTGAC	1094
O	284	ArgValPheIleProThrLysLysPhePheAsnLysGlnIleArgIubProSerLys---	302
D	1095	---TTCTTTACTGACCTCGCCACAGTTGATTATGAAACACAGCTCTCAGCGCTTGAAGACT	1154
O	303	AlaLeuLysGlnLysValSerThrAspThrLysAspLeuPheGlnLysLysIleGlyGln	322
D	1152	GCCTACACAAAGCGTGTCCCGGAAGACACAGGACAGGCTATCAGGAATGCTCGGTCAA	1211
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D	1212	AGCACCAAGCATATTGCCAAC---GGGTGACGTGATTGTGGCAAGATGATTAAAGG---	1266
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O	357	GlnGlyThrValAspPheIleAsnAsnGlnIleArgAspProSerLysAlaLeuLeuArg	376
D	1317	AAGGAGCGGTTGGACACGTTGTTGACAAAGTTAA-----TCAAAACCTTTAAAGAG	1370
O	377	LysValSerThrGlyArgLysAspLeuPheGlnLys-----LysIle	390
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QY	391	GlyGinglyThValAspPheIleAsnAsnGlu	401
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LOCUS	BBDNAD	1962 bp	DNA
DEFINITION	Babesia bigemina DNA sequence.		Linear
ACCESSION	M85187		
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ORGANISM	Babesia bigemina		
	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.		
REFERENCE	1 (bases 1 to 1962)		
AUTHORS	Mishra,V.S., McElwain,T.F., Dame,J.B. and Stephens,E.B.		
TITLE	Isolation, sequence and differential expression of the p58 gene family of Babesia bigemina		
JOURNAL	Mol. Biochem. Parasitol. 53, 149-158 (1992)		
MEDLINE	92365724		
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QY	24	AlaAlaAsnAlaIyMetIleAsnSerAspMetSerAspTyrIeuSerAlaValSerAsp	43
Db	342	GAAATGAGAGCGCTCAAGATTTACCAAGATTTGAAGATTCAAGTTGCGCAACGTCAGAG	401
QY	44	AsnPheAlaGluIuArgIleCysSerGlnValProIySgIySerAsnCysSerAlaSerVal	63
Db	402	ACCATCGTTGATGAGAGCTGTCCAGAAAGATGCTGGAACCCCTACGTGCCGCAAGAGCTA	461
QY	64	SerAlaIyrmMetSerArgCysAlaIySgIlnAspCysIeuThrIeuGlnSerIeuIyTyr	83
Db	462	ATTGCTTATGTTGACCGTTGTGATGAGGCGCATTTCTTGACGCTTGACAGCATG----	515
QY	84	ProIeuGluAlaIySgTyrGlnProIeuThrIeuProAspProTyrGlnIeuGluAlaIa	103
Db	516	-----MACTACAGCCGTTGAGTGTCCAAATCTTACCACTTGGACGCTGCC	563
QY	104	PheIleLeuPheIySgIuSerAspAlaIaAsnProIaAsnSerThrGluIyArgPheTyr	123
Db	564	TTTCATGCTTTTCAGGGAAGATGATCTTAACCTGTGGAAGATGAGGTGAACCGCTTGG	623
QY	124	MetArgPheArgValGlyIyAsnHisSerTyrPheHisAspIeuValPheAsnIeuLeu	143
Db	624	ATGCTTGTGAGG-----AGCAGCCAGCGCAGCACTACCTTGTGTGAGCTTTGG	677
QY	144	GluIySAsnValThrArgAspAlaIaSerAlaIaThrAspIleGluAsnPheAlaSerArgTyr	163
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RESULT 21
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DEFINITION Babesia bigemina DNA sequence.
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VERSION M85185.1 GI:155878
KEYWORDS
SOURCE
ORGANISM Babesia bigemina (strain Mexico) merozoite DNA.
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE 1 (bases 1 to 2005)
AUTHORS Mishra,V.S., McElwain,T.F., Dame,J.B. and Stephens,E.B.
TITLE Isolation, sequence and differential expression of the p58 gene
        family of Babesia bigemina
JOURNAL Mol. Biochem. Parasitol. 53, 149-158 (1992)
MEDLINE 92365724

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Pred. No.: 7.74e-55 Length: 2005
Score: 790.00 Matches: 170
Percent Similarity: 60.34% Conservative: 78
Best Local Similarity: 41.36% Mismatches: 133
Query Match: 33.49% Indels: 30
DB: Gaps: 10
US-09-807-459-2 (1-458) x BBDNAB (1-2005)
Oy 4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerLysValAspSer 23
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Oy 44 AsnPheAlaGluArgLecysSerGlnValProLysGlySerAsnLysSerAlaSerVal 63
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Db 678 AAGAAAGATGTTGTAACGCGACCTGATATCAATGATGTTGAGAACTGCGCATCGCAGTAC 737
Oy 164 LeuTyMetAlaThrLeuTyTrpLysThrTrpThrAsnValAspGluPheGlyAlaSer 183
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Db 738 TTCCTACATGACTACGTTGACTTACCAAGACTTACCTGACCTGCTTACGCGGCTAAG 797
Oy 184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyLysArgAlaLeu 203
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Db 798 TTCCTCAACAAGCTTGTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 857
Oy 204 LysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSerArg 223
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Db 858 AAGCGTTGGTTAGAGCAACCTCCCGTTGACCTTAGAAC---CACCTTAGGCCACC 914
Oy 224 LeuGlnHisIleThrSerSerTrpLysAspTrpMetAspThrGlnIleProAlaLeuPro 243
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Db 915 ATCCGCGAATAAGTACGCGCTACGCGAGTATGATGATGATGATGATGATGATGATGATG 974
Oy 244 LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGly 263
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Db 975 TCGTTCGCTGAGGCTTCTCCAAAGATGCTACTAGACTCTGTGTTACCTGACGAGCAG 1034
Oy 264 TyrValAspThrProTrpTrpLysTrpTrpMetLysLeuLysAsnPheMetAlaAsn 283
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Db 1035 TACSTCCATTTCGCCGCTACAGAGGTGTACAGAAATTCAAGAGATTCTATGTGCAC 1094
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 Db 1095 ---TTCTTACTGACCTGCCCAAGTGTATATGAAACGCTCTCTCAGCCTGTAAAGCT 1151
 Oy 303 AlaleuysGluLysValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGln 322
 Db 1152 GCTTACCAACAAAGCTGTGCCGGAAGACAGCAGCTATACAGAAATGTCGTGCTGAA 1211
 Oy 323 GlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLys 342
 Db 1212 AGCAACCAAGCTATATGTCCAC---GCTGTACGTATTTGGCAAGATGATTAAGAG--- 1265
 Oy 343 ValSerAsnAspAlaLysAspLeuPheGluAsnLysIle-----Gly 356
 Db 1266 -----CCTACCAACAAATTAATTCGTAGAGAGCTGCTCCTACCTTTCTAAGCA 1316
 Oy 357 GlnGlyThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArg 376
 Db 1317 AAGGAGCGCTTGAGCAGCTGTGTACAAAGCTTAA-----TCAAAACCTTTAAGAG 1370
 Oy 377 LysValSerThrGlyAlaGluAspLeuPheGluAsn-----LysIle 390
 Db 1371 CGTCTGTGTAATCATCGAAGAAATCATACAGGATTCCTCAAGAAATTCCTCAAGAA 1430
 Oy 391 GlnGlnGlyThrValAspPheIleAsnAsnGlu 401
 Db 1431 TCACATATATATTCAGATCCGCAAAATCATATGAG 1463
 RESULT 22
 AL6434 1371 bp DNA linear PAT 23-MAR-1994
 LOCUS (lambda GEM-11 #9) gene 2 encoding a 211B4/rhoptry protein
 DEFINITION homologue.
 VERSION A16434
 KEYWORDS A16434.1 GI:511983
 SOURCE Babesia canis.
 ORGANISM Babesia canis.
 Eukaryote; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
 Babesia.
 REFERENCE 1 (bases 1 to 1371)
 AUTHORS BABESIAL ANTIGENS
 TITLE Patent: WO 9314204-A 13 22-JUL-1993;
 JOURNAL Location/Qualifiers
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 BASE COUNT 418 a 312 c 325 g 316 t
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 Alignment Scores: 1,84e-53 Length: 1371
 Pred. No.: 770.50 Matches: 161
 Score: 770.50
 Percent Similarity: 55.65% Conservative: 95

Best Local Similarity: 35.00% Mismatches: 161
 Query Match: 32.66% Indels: 43
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 Oy 1 MetaIaProSerAspSerValGlyAspValThrLysThrLeuAlaIaSerGluSer 20
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 Oy 21 ValAspSerAlaIaAsnAlaTyMetIleAsnSerAspMetSerAspTyLeuSerAla 40
 Db 151 ACGAGAGCGGCTTTAGAGAGCGCTACAGAAATGATCTGCTATAGGCAACTTTTCAACGGT 210
 Oy 41 ValSerAspAsnPheAlaGluArgIleCysSerGlnValProlGlySerAspCysSer 60
 Db 211 CGCAGCGAAGAGAGAGAGAGAGAGAGCTGTCTGTGAACATCGCAGAGACATGATGTCAG 270
 Oy 61 AlaSerValSerAlaTyMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer 80
 Db 271 AAGAGCGTACGTGATGATGTGAAGCGTCCGACGATGACGCTTATGACATTGAGAC 330
 Oy 81 LeuLysTyProLeuGluAlaLysTyGlnProLeuThrLeuProAspProTyGlnLeu 100
 Db 331 CAGAACTCCTCAAG 390
 Oy 101 GluAlaIaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLys 120
 Db 391 GAGGCGCGCTTCTATGCTTGTGAGAAACGATGATCAACCAATTTAAACCAACGAA 450
 Oy 121 ArgPheTrpMetArgPheArgGlyLysAsnHisSerTyPheHisAspLeuValPhe 140
 Db 451 GCTTCTGTGATGCTTTCGTCACGCGAGCATGATGCGCTTCAACATTTCTGTGTG 510
 Oy 141 AsnLeuLeuGluLysAsnValThrArgAspAlaIaPheAlaThrAspIleGluPheAla 160
 Db 511 AATATCTATATTAACAACTCAGCATGATGATGATGATGATGATGATGATGATGATGATG 570
 Oy 161 SerArgTyLeuTyMetAlaThrLeuTyTyTrpLysThrTyTrpAsnValAspLuphe 180
 Db 571 CGCAATATGCTTACATGCGCACCATGATATCAAGACATACACCGCTTGGATGTTGTA 630
 Oy 181 GlnLysSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyLys 200
 Db 631 AATCCAGCATCATTAACAAATTCCTTCGCCGCACTGTCGGAAGCAATTAAGC 690
 Oy 201 ArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGlnHisSer 220
 Db 691 AACGCCCTAACGAATATATATCCGAGTACATTCGCCGAGACTTCGGC--AAGTACAC 747
 Oy 221 ValSerArgLeuGlnHisIleThrSerSerTyTrpLysAspTyTrpMetAspThrGlnIlePro 240
 Db 748 GTTGACCGCTGAGAGCAGCATGATGGTGGCTACAGAGGATCATGATGAACCAAGTACCA 807
 Oy 241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr 260
 Db 808 TCTCTTCCAAATTTCCGCAAGAAATACCGGGGAATGGTGAAGAGATTATTAAGAAAT 867
 Oy 261 ValAlaGlyTyTrpValAspThrProTyTrpLysLysTyTrpTyMetLysLeuLysAsnPro 280
 Db 868 GTGGAGCTTACCAAGAACACCATGTTCAAAAAGCTGAACAATCAATATGAAGAACTTC 927
 Oy 281 MetValAsnArgValPheIleProThrLysLysPhePheAsnLysGluIleArgLupro 300
 Db 928 TTCTGTAACCAAGATCCATGAACCCACCAAGAGATTTCTTCGTAACCAAGATCCATGAACCC 987
 Oy 301 SerLysAlaLeuLysGluLysValSerThrAspThrLysAspLeuPheGluAsnLysIle 320
 Db 988 -----ACCAAGAGATCTTCGTGACCAAGATC 1014
 Oy 321 GlnGlnGlyThrValAspPheAsnLysGluIleArgAspProSerLysAlaLeuLys 340
 Db 1015 CATGAACCCACCAAGAGAGATTTCTTCTGTGAACAAAGATCATGAACCCACC----- 1062

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Oy 341 GluIyValSerAsnAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrVal 360
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Oy 361 AspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValSerThr 380
Db 1102 GAGTTCCTTCGTGACACAGCTCCACGACCAAGAGTTCCTTCGTACACATGGTGAACC 1161
Oy 381 GlyAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsn 400
Db 1162 GGGGCAATCCAGACAGATATCTGAAAGAGCGAGCTAGA----- 1197
Oy 401 GluIleArgAspProSerLysAlaLeuIleArgLysValThrThrGluAlaAspLeu 420
Db 1198 CACCTGACAGAGT---CTTAAGACAGCTGTCCCTGAA-----GACGAGCCCTCATCTCT 1248
Oy 421 PheGluAsnLysIle-----GlyGlnGlyThrVal---AspPheIleAsnLysGlu 436
Db 1249 CTGGAATAATGAGCGTGTAGAGGATGTCACATTAATGGGGGATGTGACGATTTTGAA 1308
Oy 437 IleArgAspPro-----SerLysAlaLeuIleArgLysValSerThrGlu 451
Db 1309 ATGGGACTCCACCTATGAGCAGGCGTCACAGAGATTTAATGAAGTGTGTAACGAA 1368

RESULT 23
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DEFINITION Babesia canis putative (60.2) rhoptry protein gene, complete cds.
ACCESSION M91168
VERSION M91168.1 GI:155908
KEYWORDS rhoptry protein.
SOURCE Babesia canis (strain Tomsville) DNA.
ORGANISM Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.
REFERENCE 1 (bases 1 to 2796)
AUTHORS Dairymple,B.P., Casu,R.E., Peters,J.M., Dimmock,C., Gale,K.R.,
Bose,R. and Wright,I.G.
TITLE Characterisation of a family of multi-copy genes encoding rhoptry
protein homologues in Babesia bovis, Babesia ovis and Babesia canis
JOURNAL Mol. Biochem. Parasitol. 57, 181-192 (1993)
MEDLINE 93165069
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Oy 21 ValAspSerAlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla 40
Db 1180 ACGAGACCGCTTATGAAAGCTACAGAAATGCTGCTATGCGCAACCTTTCACAAACGCT 1239
Oy 41 ValSerAspAsnPheAlaLeuArgIleCysSerGlnValProLysGlySerAsnGlySer 60
Db 1240 CCGAGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1299
Oy 61 AlaSerValSerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer 80
Db 1300 AAGAGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1359
Oy 81 LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeu 100
Db 1360 CAGAAATACCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1419
Oy 101 GluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProLysAsnSerThrGluLys 120
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Oy 121 ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe 140
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Oy 201 ArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGlnHisSer 220
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Oy 221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIlePro 240
Db 1777 GTTGACCGCGCTGAGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1836
Oy 241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr 260
Db 1837 TCTCTTCAAAATTTCCCAAGAAATACGCGGGAATGCTGTAAGAGTTTAATTAAGAAT 1896
Oy 261 ValAlaGlyTyrValAspThrProTyrTyrLysTyrTyrMetLysLysAsnPhe 280
Db 1897 GTGGGAGCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1956
Oy 281 MetValAsnArgValAlaPheIleProThrLysPhePheAsnLysGluIleArgGluPro 300
Db 1957 TTTCGTAAACAGATCCATGACCCACCAAGAGATTTCTTGTGACAAAGATCCATGAAACC 2016
Oy 301 SerLysAlaLeuLysGluLysValSerThrAspThrLysAspLeuPheGluAsnLysIle 320
Db 2017 -----ACCAAGAGTTCCTTCGTGACCAAGATC 2043
Oy 321 GlyGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeuLys 340
Db 2044 CATGAACCCACCAAGAGATTTCTTCGTGACCAAGATCCATGAAACCAC----- 2091

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Alignment Scores: 4.37e-53 Length: 2796
 Pred. No.: 770.50 Matches: 161
 Score: 55.658 Conservative: 95
 Percent Similarity: 35.00% Mismatches: 161
 Best Local Similarity:

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Db	2092	-----AAGAGATTTCTTCGTGAACAGCTCCATGAAACCCACCAAG	2130												
Oy	361	AspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValSerThr	380												
Db	2131	GAGTTCTTCTGTAACACAGCTCCATGAAACCCACCAAGAGTTCTTCTGTAACATGGTACC	2190												
Oy	381	GIyAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsn	400												
Db	2191	GGCGCATTCACGAAGATATCTGAAAGACGACGAGTAGA-----	2226												
Oy	401	GluIleArgAspProSerLysAlaLeuIleArgLysValTyThrGluAlaAspAspLeu	420												
Db	2227	CACCTGAGAACT--TCTAAGACACTTGTCCCTGA-----GACGACCCCTCATCGTCT	2277												
Oy	421	PheGluAsnLysIle-----GlyGlnGlyThrVal--AspPheIleAsnLysGlu	436												
Db	2278	CTGGAAGATGAGAGCTGTAGAGATGTGTCACTTACAAATGGGGATGTGACCATTTTGAA	2337												
Oy	437	IleArgAspPro-----SerLysAlaLeuIleArgLysValSerThrGlu	451												
Db	2338	ATGGCGACTCCACCTATGAGCAGCGGCTCACAGAGAGACTTAAATGAAGTTGTTAAGCAA	2397												
LOCUS	A16432	1491 bp	DNA	linear	PAT 23-MAR-1994										
DEFINITION	(Lambda EMBL3 #5) gene 5 encoding 21B4/rhoptry homologue.														
ACCESSION	A16432														
VERSION	A16432.1	GI:511981													
KEYWORDS	Babesia ovis.														
SOURCE	Babesia ovis														
ORGANISM	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.														
REFERENCE	1 (bases 1 to 1491)														
AUTHORS	BABESIAL ANTIGENS														
TITLE	Patent: WO 9314204-A 11 22-JUL-1993;														
JOURNAL	Location/Qualifiers														
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Qy	21	ValAsSerAlaIaIaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrIleuSerAla	40
Dd	151	ATAAATGCCGAAACATGAGACATGAATAAATGATGATGCTATTAAACACTGGTAGA	210
Qy	41	ValSerAspAsnPhenIleuIleuArgIleCysSerIleValProlySGlySerAsnCysSer	60
Dd	211	GAGGGAAGTAAATTTATTTGATCAAAATTTGTCAGGAACCTCCCTGGAGTCTTAAGTGGCGT	270
Qy	61	AlaSerValSerAlaTyrMetSerArgCysAlaIleCysIleAspCysIleuThrIleuGlnSer	80
Dd	271	GAACAAGTTGATCATCTATATGTTAACCCGTTTGACAGAGAACAACTTTTACAGATTGACGA	330
Qy	81	IeuLysTyrProIleuGluAlaIleuPheLysGlyIleProIeuThrIleuProAspProIeuGlnIleu	100
Dd	331	GTAGCTTACCCCTTGGAATCAGGAATATCAGCCACTATTACTCCGGAAACCATCAAAATTC	390
Qy	101	GIuAlaIaIaPheIleuPheLysGluSerAspAlaAsnProAlaAsnSerThrIleuLys	120
Dd	391	GATGCTGCCTTCACATTTGCTTCACAAACCTGCAGCTCATATCTGCTTAAATAATGGCCGTGAA	450
Qy	121	ArgPheTrpMetArgProPheArgArgGlyLysAsnHisSerTyrPheHisAspIleuValPhe	140
Dd	451	GGTCCATGATGATCGCTTACAAAGAGGTAAGACATGCTGACTACACCACTTTCATCATATA	510
Qy	141	AsnIleuGluGlyLysAsnValThrArgAspAlaIaAspAlaThrAspIleuGluAsnPheAla	160
Dd	511	AGTTTGCTCGGCAGAGAGTTTGTCGTAAAGATGCTGTACTGACCTTGAGTTCCCTGCTC	570
Qy	161	SerArgTyrIleuTyrMetAlaThrIleuTyrTyrLysThrTyrThrAsnValAspGluPhe	180
Dd	571	AACAAGCTTTTGTCATGATGGCCACACCACTACTACCAAAACCTCAATTTGTCAGAAAGATTC	630
Qy	181	GlyAlaSerPhePheAsnLysLeuSerPheThrIleuPheGlyTyrPglyIleLys	200
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Dd	691	AGGGCATTTAAAGGATCGTCCGCTCCATGTTCCGGAAGACATGGGA---GAGCACAGT	747
Qy	221	ValSerArgIleuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIlePro	240
Dd	748	ATTGAAGCTATTAGCATTTGTCGGAAGATACCAAGACATCAATGTTGACAGAGTGGCCA	807
Qy	241	AlaIleuProLysPheAlaLysArgPheSerIleuMetValValGlnArgIleuAlaIaThr	260
Dd	808	ACCCCTTCAAGGTTGGCCGAACGTTACTCTGACATGGTATTGAAGAATTCTGGTTGAGCAGC	867
Qy	261	ValAlaGlyTyrValAspThrProTrpTyrLysLysTyrPyrMetCysIleuLysAsnPhe	280
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Qy	281	MetValAsnArg-----ValPheIle	287
Dd	928	TTAACTGTGTAAGCTTACACCTGATGAGAAATATACATTACTTAAACCTATTATTTCGTT	987
Qy	288	ProThrLysLysPhePheAsnLysGluIleArgIleuProSerLys---AlaIleuLysGlu	306
Dd	988	GATACTCTCAGGAATTAATCATAAAGATGACCTTAAGCCACTGCTGATGCTGTAGAGGAA	104
Qy	307	LysValSerThrAspThrLysAspLeuPheGluLysAsnIleGlyGlnGlyThrValAsp	326
Dd	1048	AATATCTGTTAAACCCGCTGATGATTAATCTCCGACGCAAGCAAAATATTCTAGTCAACA	110
Qy	327	PhePheAsn-----LysGluIleArgAspProSerLysAlaIleu	339
Dd	1108	AACATCATGACGGGCAATCAAAATAGATCCCTCTTATTAAGAACTTAAGAGCGGCAT	116
Qy	340	LysGluLysValSerAsnAspAlaLysAspLeuPheGluLysAsnLysIleGlyGlnGlyThr	359

DB 1168 ATCGGAATTGCTGCGAATCAGCTAGCATATATAGATGATAAGGTAATAA----- 1221
OY 360 ValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValSer 379
DB 1222 -----GCCAAGAAATTAAGTCCGCGCCAG 1248
OY 380 ThrGlyAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsn 399
DB 1249 GACCCGCGACAGCGCATATATGACATGCGTAACCTGCTGATGATATTTACGAAC 1308
OY 400 -----AsnGluIleArgAspProSerLysAlaLeuIleArgLysValTyr----- 414
DB 1309 GTTGTAAAGAAATGATCTTCTTGTGACGTAAC-----ATCAGAAATATATTAAGTGGC 1362
OY 415 ---ThrGluAlaAspAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIle 433
DB 1363 ACCTCTCAAGATGACATATATGACAAAGAAAGACTGAGAGAGAAAGTTGAGAAATT 1422
OY 434 AsnLysGluIleArgAspProSerLysAla 443
DB 1423 AAACCTGACCTGACGAAAGAAAGATATGCT 1452
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LOCUS Babesia ovis putative (60.4 and 60.5) rhoptry protein genes, 3' end
DEFINITION and complete cds respectfully.
ACCESSION M91169.1 GI:155900
VERSION M91169.1 GI:155900
KEYWORDS rhoptry protein.
SOURCE Babesia ovis (strain Ankara) DNA.
ORGANISM Babesia ovis
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.
1 (bases 1 to 4145)
Dairymple,B.P., Casu,R.E., Peters,J.M., Dimmock,C., Gale,K.R.,
Bose,R. and Wright,I.G.
Characterisation of a family of multi-copy genes encoding rhoptry
protein homologues in Babesia bovis, Babesia ovis and Babesia canis
Mol. Biochem. Parasitol. 57, 181-192 (1993)
93165069
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/db_xref="taxon:5869"
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BASE COUNT 1341 a 813 c 846 g 1145 t
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OY 61 AlaserValSerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer 80
DB 2402 GAACAAGTTGAATCATATATGATTAAGCTTTGAGAGAACACAGCTTTACAGATTGACGA 2461
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OY 121 ArgPheThrMetLysPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe 140
DB 2582 GGTCCATGGATGGCTTACCAAGAGGAGTAAGACATGGTACATCCCATTTCAATCA 2641
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DB 2702 AACCAACCTTTTGTACATGGCCACACCTACTACAAAACCTAATTGTCAAGAAATTG 2761
OY 181 GluAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrPglYIleLys 200
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DB 2939 ACCCTTTCAAGATTTGCGCAAGCTTACTGACATGTTATGAAGCTTGTGGACACAC 2998
OY 261 ValAlaGlyTyrValAspThrProTyrTyrLysTyrPheMetLysLeuLysAsnPhe 280
DB 2999 CTCGCGGTTATATCAAGGCTCATGTTACAAAGATGATGATCAATGATTAAGTCTCTG 3058
OY 281 MetValAsnArg-----ValPheIle 287
DB 3059 TTAACGTGGAAGCTTACAACACCTGATGAAGATATATGATTAACCTATTTTCGTT 3118

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OY	307	LysValSerThrAspThrLysAspleuPheGluAsnLysIleGlyGlnGlyThrValAsp		326
Db	3179	AATATCGTTAAACCCCGTCAGTGATTTATCTCCGACGACCAAAAATATTTCGTACACA		3238
OY	327	PhePheAsn-----LysGluIleAspProSerLysAlaLeu		339
Db	3239	AACTACATGACGGGCATCATTAAATAGATCCCTCTTTTAGAACCTTAAGGCCGAT		3298
OY	340	LysGluLysValSerAsnAspAlaLysAspleuPheGluAsnLysIleGlyGlnGlyThr		359
Db	3299	ATCGCAATTCCTCCGAATCACGCTGAGGATTTATATAGATGATTAAGCTAAATTA--		3352
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Db	3353	-----GCCAAAGATTTAGTCCGCTCCCAAG		3379
OY	380	ThrgLysIleGluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsn		399
Db	3380	GACCCGCAACAGCATATATGCAGATCATCGGAAACCTGCTCTAGCATTTTACGAAC		3439
OY	400	-----AsnGluIleArgAspProSerLysAlaLeuIleArgLysValTrp----		414
Db	3440	GTTTGTAAGAATGATCTTCTGATGTCAGATAAAC-----ATCAGAAATATATTACGTGC		3493
OY	415	---ThrgLysIleAspAspleuPheGluAsnLysIleGlyGlnGlyThrValAspPheIle		433
Db	3494	AGCTCTCAAGATGACAAATATGAAACAGACAGACTGACGAGAGAGAAGTGAAGAGATT		3553
OY	434	AsnLysGluIleArgAspProSerLysAla		443
Db	3554	AAACCTGAGCTGAACCAAAAGATATGCT		3583
RESULT 26				
EBORAIIP				
LOCUS		2549 bp	DNA	linear
DEFINITION	Babesia bovis (clone 4-1) rhoptry associated protein 1 (RAP-1) gene,			
	1, 3' end of cds, rhoptry associated protein 1 (RAP-1) gene 2,			
	complete cds.			
ACCESSION	L77326			
VERSION	L77326.1			
KEYWORDS	GI:1256656			
SOURCE	rhoptry associated protein 1.			
ORGANISM	Babesia bovis (strain Mo7) (clone: 4-1) DNA.			
	Babesia bovis			
	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;			
	Babesia.			
REFERENCE	1 (bases 1 to 2549)			
AUTHORS	Suarez,C.E., Palmer,G.H., Hines,S.A. and McElwain,T.F.			
TITLE	The Babesia bovis rhoptry associated protein-1 intergenic region			
JOURNAL	encodes a functional eukaryotic promoter			
FEATURES	Unpublished (1996)			
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[illegible]

Accession	Source	Organism	Location/Qualifiers
DB 539	AAAGATGATGAAGAATTCAGAGATTTTCTCTAATAAACGTTACCAACTCAAG		598
OY 291	Lysphe-----		292
DB 599	AAGTTCATCGAGGACTAAGCAAGTATCCAAAACTATCTGAAGCCATGTTCGAG		658
OY 293	-----Pheasnlyslu		296
DB 659	CCCACTAAAAAGTTATGCGAGACACTACGAAAAAACCAAGGCTATCTGAAGAGAT		718
OY 297	llearggluproserlyslaleuylsgluylsvalserthraspserlyslaspleu		316
DB 719	GTAGCCGAACCTACTAATACTTTTTCAGAGAGGCTCCTCAAGTACCAAAACACTTTC		778
OY 317	gluasnllyslleagllynglylthrvslasppheasnllyslleagllynglylthrvslasp		336
DB 779	GATGAGAACATTTGGCCCAACCCCAAGGAGTTTTCAGGAAAGCTCCCAAGCCACTAA		838
OY 337	lysAlaleuylsgluylsvalserthraspserlyslaspleuylsAlaleuylsleely		356
DB 839	CATTCTCTAGACGAACATCGGTCAACCAACCAAGAGGTTCTTC--AGGAGGCTCCT		895
OY 357	glnglylthrvslasppheleleasnslnglylthrvslaspproserlyslaleuyllearg		376
DB 896	CAAGCACTAAGCACTCTCTAGCGAGAGATATGTCTCAACTACTAATAAGATTTTTCAG		955
OY 377	lysvalserthrglylalaqluaspleuylsleagllynglylthrvslasp		396
DB 956	GATGCTCCTCAAGTACCAAGAGGTTATTAAGTGAAGACATTTGCTCAACCAACTAAGG		1015
OY 397	Phe-----lleasnslnglylthrvslasp		405
DB 1016	TTCTTTAGGAGGTTCTCATGCTACATGAAGTCTTGAATGAAGAACTGCTCAACCT		1075
OY 406	serlyslaleuyllearglylthrvslalysvalthrglylthrvslaspleuylsleely		425
DB 1076	GCCAAAGAAATCATCATGAGCTTGCTGACAGCGCCAAAGAT--TTATCTCGGCACCC		1132
OY 426	glnglylthrvslasppheleleasnslnglylthrvslaspproserlyslaleuylle		445
DB 1133	CATGAAGTACTAAGCACTCTTAAACGAACCTGTGGCCAAACCTAACAAGAAATTCCTG		1192
OY 446	Arg--Lysvalserthrglylthrvslaspleu		455
DB 1193	AACGAGCTTTAGAAACTACTAAGACCCACTTA 1225		
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DEFINITION	Babesia ovis putative (60.2 or .3) rhoptry protein gene, 5' end and		
ACCESSION	putative (60.3 or .4) rhoptry protein gene, 3' end.		
VERSION	M91173		
KEYWORDS	M91173.1 GI:155917		
SOURCE	rhoptry protein.		
ORGANISM	Babesia ovis (strain Ankara) DNA.		
	Babesia ovis		
	Eukaryota; Alveolata; Apicomplexa; Phloplasmida; Babesiidae;		
	Babesia		
REFERENCE	1 (bases 1 to 2851)		
AUTHORS	Dalrymple,B.P., Casu,R.E., Peters,J.M., Dimmock,C., Gale,K.R.,		
TITLE	Bose,R. and Wright,I.G.		
JOURNAL	Characterisation of a family of multi-copy genes encoding rhoptry		
MEDLINE	protein homologues in Babesia boyds, Babesia ovis and Babesia canis		
FEATURES	Mol. Biochem. Parasitol. 57, 181-192 (1993)		
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Db	4	TTGTACATGGCCACCACTATTACAAAACCTAATGTGCACAAACAGCGATGCCAA	632.50	Matches: 136	Conservative: 49	Mismatches: 90
Db	184	PhepheaLnLysSerPheThrThrGlyLeuPheGlyIleTyrsArgAlaLeu	632.50	Matches: 136	Conservative: 49	Mismatches: 90
Db	64	TTCTTTACAGAGATTGCTTTCGCAACAAGATTTTCGGTTTGGTATCAAGAGCGCTC	26.81%	Indels: 18	Gaps: 6	
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Db	124	AAGGATATTCGTCGCTCCAAATGTTCCCGAATATATGGAA--GAGCACAGATTGAACG	180			
Db	224	LeuGlnHisIleThrSerSerTyrrLysAspIrrMetAspThrGlnIleProAlaLeuPro	243			
Db	181	ATTAGTCATTTGGCCACCGTTTACAAAGCATACATGTTGACCCCAAGTCCCAACCTTTCA	240			
Db	244	LysPheAlaTyrsArgPheSerLeuMetValAlaGlnArgLeuAlaThrValAlaGly	263			
Db	241	AAGTTTCCGCAACGCTTACTGTGACATGGTTATGAAAGTCTGTTGACACGCTGCCGCT	3000			
Db	264	TyrValAspThrProTrrPrrLysLysTrpIrrMetLysLeuLysAsnPheMetValAsn	283			
Db	301	TATGTCAAGGCTTCATGATGATACAAAGAGATGTTTCAAAAGGTTAAAGATTCTTGTAAAC	360			
Db	284	ArgValPheIlePrrCrrThrLysLysPhePheAsnLysGlnIleArgGluProSerLysAla	303			
Db	361	AAAAATAGCAACCTACAAAGAAACACTTCCACAAAG-----AAACACCCACGACCGCC	414			
Db	304	--LeuLysGlnLysValSerThrAspThrLysAspLeuPheGlnAsnLysIleGln	322			
Db	415	GAATTTTTCGCAAGATGATGCAAGAACGACCAAGAGATCTTTCGAGAAACAGATAGTGCT	474			
Db	333	GlyThrValAspPhePheAsnLysGlnIleArgAspProSerLysAlaLeuLysGlu--	341			
Db	475	CCTACCAAGGACTTCTTTCGAGAACAGATAGTACTCTCCTACCAAGGACTTCTTTCGAGAAC	534			
Db	342	LysValSerAsnAspAlaLysAspLeuPheGlnAsnLysIleGlnGlnGlyThrValAsp	361			
Db	535	AAGATAGTGTCTCTACCAAGGACTTCTTTCGAGAACAGATAGTACTCTCCTACCAAGGAC	594			

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OY	383	AlAglASPlaePheGlUnASnLylleGlYngInGlyThrValASpPheIlleaSnAnGlu	401
Dd	628	-----GACTTCTTTGAGAACAAGTAGGTGCTCCTACCAAGACTCTTGCAGAAACAAG	681
OY	402	IleArGAsProSeRlYSAlAlLeUlle---ArGlYSValTYThrGUAlASpspleu	420
Dd	682	CtGGCTGAAGCACCAAGGACTCTTCGAGAACCAAGCTCCGAAACACCAAGGACTTC	741
OY	421	PheGUASnLylleGlYngInGlyThrValASpPheIlleaSnLylleArGAsPro	440
Dd	742	TTCGAGAACAAACCTCGCTCAACACACCAAGACTCTTTGAGAACAAAGTTGCTGCCCC	801
OY	441	SerLYsAlAlLeUlIleArGlYSValSerThrGUAlA	452
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DEFINITION	B.divergens mRNA for rhoptry associated protein.		
ACCESSION	Z49818		
VERSION	Z49818.1 GI:974766		
KEYWORDS	rhoptry associated protein.		
SOURCE	Babesia divergens.		
ORGANISM	Babesia divergens Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia. 1 (bases 1 to 1483) Skuce,P.J., Mallon,T.R. and Taylor,S.M. Molecular cloning of a putative rhoptry associated protein homologue from Babesia divergens Mol. Biochem. Parasitol. 77 (1), 99-102 (1996)		
REFERENCE	2 (bases 1 to 1483)		
AUTHORS	Skuce,P.J.		
TITLE	Direct Submision		
JOURNAL	Submitted (10-APR-1995) Skuce P. J., Department of Agriculture for Northern Ireland, Veterinary Sciences Division, Stonely Road, Stormont, Belfast, Northern Ireland, BT4 3SD		
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LOCUS      Babesia bigemina RAP-1c (rap-1c) gene, complete cds, and
DEFINITION YJ0700c-like protein (YJ0700c-like) gene, partial cds.
ACCESSION  AF026272
VERSION     AF026272.1  GI:2583051
KEYWORDS
SOURCE      Babesia bigemina.
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ORGANISM    Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 4414)
AUTHORS    Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE      Genomic cloning of Babesia bigemina rap-1c gene
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 4414)
AUTHORS    Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE      Direct Submission
JOURNAL    Submitted (22-SEP-1997) Department of Veterinary Microbiology and
            Pathology, Washington State University, Pullman, WA 99164-7040, USA

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BASE COUNT      1213 a      1030 c      1087 g      1082 t      2 others

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DB:              3      Gaps:      15

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Oy      134  TyrPheHisAspLeuValPheAsnLeuGluLysAsnValThrArgAspAlaAspAla 153
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Db      1510 GCTTACTACAGCTTTCAGCTTCACACCTGTGAGCGCAACCTGTTCTCGCGCAGCAACAA 1569

Oy      154  ThrAspIleGluAsnPheAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThr 173
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Db      1570 AATGCCCTCATGCTTCGTGCAAGAGTACTTTCATATGACCGCCATATATCAAGAGCA 1629

Oy      174  TyrThrAsnValAspGluPheGlyAlaSerPheAsnLysLeuSerPheThrThrGly 193
          |||
Db      1630 TACTTTCGCTGATGCCATCAACGCCCAAAATTTTAACAAATTCGCTTGGCGGAAGCAC 1689

Oy      194  LeuPheGlyTyrPylLysAlaGalaLeuLysGlnIleIleArgSerAsnLeuProLeu 213
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Db      1690 ATTCTGGACCTTAAGATCAAAAGGCGTTGAGGAAGATGCTGCAGGCAACAGCCGAC 1749

Oy      214  AspIleGlyThrGlnHisSerValSerArgLeuGlnHisIleThrSerSerTyrLysAsp 233
          ::|||
Db      1750 GCGCTC---CAAGCAAGCAGCTCAAGCCATAGCGCCCTTACGCTTACAGGCAAG 1806

Oy      234  TyrMetAspThrGlnIleProAlaLeuProLysPheAlaLysArgPheSerLeuMetVal 253
          |||||
Db      1807 TACATGGCAACCAATTCATCGCTTCCTTTCGCTTACGCTTTCCTTCGATGATGCT 1866

Oy      254  ValGlnArgLeuLeuAlaThrValAlaGlyTyrValAspThrProTyrLysLysTyr 273
          ::|||
Db      1867 GTCACCGCTCTGCTGACCAACCTCACCAGGCTTAACAGACAGCGCGGTACAGAGCTGG 1926

Oy      274  TyrMetLysLeuLysAsnPheMetValAsnArgValPheLeuProThrLysLysPhePhe 293
          ::|||
Db      1927 TTGGAAAGGTGAAGACCTTTCACCGGTAAACAA-----CCAGCGAAAGGCGCTTAC 1980

Oy      294  AsnLysGluIleArgGluProSerLysAlaLeuLysGluLysValSerThrAspThrLys 313

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Db 1981 -----GAAATTGACGAACCCATCGCCACCGAGGAG-----ACCGAG 2019
Oy 314 Aspleuphagusnlyslleglyglnglythryalasphepneanlysllearg 333
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Oy 334 Asproserlysalaleuylslulysvalserasn-----345
Db 2053 -----GTCACGAGAAAGCTTGCAACATCCGCTTCACACGCGCATTTTC 2097
Oy 346 -----Aspalalyt-----348
Db 2098 CGAAAGGCTGAGCAAGACTGCTACTCGACCTTTCCGAGAGACATTATGGCAGC 2157
Oy 349 -----Aspleuphagusnlysllegly 356
Db 2158 TTTCGTCGCTGATGCGCTCTTGAGCCGCTGCTCGATGTCATGGAG---AAAGAGGCC 2214
Oy 357 Glncllythryalaspheileasnangluileargasproserlysalaleuilearg 376
Db 2215 GAACCTCAG-----ACGAGGAGGAGGTGAACCGAAGTGGCGGCTCC 2262
Oy 377 Lysvalser-----Thnglyalagluaspleu 385
Db 2263 AAGCGCTGAGACTGAAATGCGCAACTCGCAGACCAAGTAGATGTGCTTCAACTGTG 2322
Oy 386 Pheglusnlyslleglyglngly-----Glythryalasphe 397
Db 2323 GCTCAACGGAATGGGGAAGAGAGATCTCGAAGCTCTTAAGGACCGCAGATTG 2382
Oy 398 Ileasnangluileargasp-----Proserlysalaleuile 410
Db 2383 ATGCACGAAGATGAGCAGCAAGCAATCTGACGAATTCCTGCCACAGCAAGCGT 2442
Oy 411 Arglysaltyrthnglualeaspheupheglusnlyslleglyglnglythryal 430
Db 2443 AAGCTTCACACAGGCTTACAAAGATTCTTCAGAAACTCTTGACACCGGTGCATT 2502
Oy 431 Aspheileasnlyslleargasproserlysl 442
Db 2503 AAGATGCCGCTAGCCGATGGGTCCCGAAGAG 2538

RESULT 30
AF014757 575 bp DNA linear INV 31-JAN-2001
LOCUS Babesia bigemina CGA rap-1 alpha (rap-1) gene, partial cds.
DEFINITION AF014757
ACCESSION AF014757.1 GI:2429255
VERSION
KEYWORDS
SOURCE Babesia bigemina.
ORGANISM Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.
REFERENCE 1 (bases 1 to 575)
AUTHORS Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
JOURNAL loci of Babesia bigemina
MEDLINE MCL Biochem. Parasitol. 90 (2), 479-489 (1997)
98135662
REFERENCE 2 (bases 1 to 575)
AUTHORS Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1997) Department of Veterinary Microbiology and
Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES
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TLVYKTYLVDFEPAKFFNKLAFTTRLEFG"
BASE COUNT 145 a 119 c 153 g 158 t
ORIGIN
Alignment Scores:
Pred. No.: 1.24e-34 Length: 575
Score: 532.00 Matches: 103
Percent Similarity: 69.23% Conservative: 32
Best local Similarity: 52.82% Mismatches: 52
Query Match: 22.55% Indels: 8
DB: 3 Gaps: 2
US-09-807-459-2 (1-458) x AF014757 (1-575)
Oy 4 SeraspservValglYaspvalThrlYsThrluLeuAlaIasengluSerValasps 23
Db 14 GCAGAGGTGTGGAGATGTGTCCAGACTTGGCTGGAGGCCAATGAGCTGTGCAATGCT 73
Oy 24 AlaIaasnaIatYrMetIleasnSeraspMetSeraspTyrluSerAlaIas 43
Db 74 GAATGCAAGACACTCAGCTCAACAAAGATATGCAAGATCAATGTCAATGTAAAGAG 133
Oy 44 AsnPhaIaIaIuargIlecySerelInValProlysglySeranCySerAlaSer 63
Db 134 ACCATTGTGGTGAGGCTCGCAGCAAGTCTGGAACCTGACTGCGGTGAGAGCGTA 193
Oy 64 SerAlatYrMetSerarCyAlaIySglnasPcySleuThrluSglInserIystr 83
Db 194 ATTGCTTATGTTAACCGTTGTGATGAGGCGATTGTCTGACGCTTGACAGCATG 247
Oy 84 ProleugluAlaIystrGlnProleuThrluProaspProtyrGlnleuGluAla 103
Db 248 -----AAGTACAGCCGTTGAGTCTGCCAATTCCTACAGTGGAGCGTCC 295
Oy 104 PheileuPheIySgluSeraspAlaasnProIaasnSerThngluYargPheItr 123
Db 296 TTCAATGCTTTTCAGGGAAGATTCATACCTCGGAAGATGAGCTAACCGCTTCG 355
Oy 124 MetIargPheIargGlyIyasnHisserIyPheIIsasPleuValPheasnleu 143
Db 356 ATGCGTTGAGG-----ACGAGCCGCGCAGCACTACCTACTTGTGTGTTGCTTGG 409
Oy 144 GluIyasnValThrIargaspAlaaspAlaThrasPilegluasPheIasSerArg 163
Db 410 AAGAAGATGTGTGACGCGCAGCCGCAATCAATGATGTGAGAACTTGCGACGATAC 469
Oy 164 LeuYrMetAlaThrluLeuTyrlYslYsThrYrThrasnValaspGluPheglYAlaser 183
Db 470 TTTCACACGACTGACTGTACTACAGACTTACCTGACCGTTCGCTTACGCGCTAAG 529
Oy 184 PhePheasnlysluSerPheThrlYsThrluPheglYtrpgly 198
Db 530 TTCTTCACACAGCTTGCTTTCACACACTGCTGTGCTTGGT 574

RESULT 31
AF014758 575 bp DNA linear INV 31-JAN-2001
LOCUS Babesia bigemina CGP rap-1 alpha (rap-1) gene, partial cds.
DEFINITION AF014758
ACCESSION AF014758.1 GI:2429257
VERSION
KEYWORDS
SOURCE Babesia bigemina.
ORGANISM Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.
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REFERENCE 1 (bases 1 to 575)
AUTHORS Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
loci of *Babesia bigemina*
JOURNAL Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
MEDLINE 98135662
REFERENCE 2 (bases 1 to 575)
AUTHORS Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1997) Department of Veterinary Microbiology and
Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES
source location/Qualifiers
1..575
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gene <1..>575
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CDS <1..>575
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TLVYKTYLTVDFTAKFNFKLAFTRLFEGF"

BASE COUNT 145 a 119 c 153 g 158 t
ORIGIN

Alignment Scores:

Pred. No.:	1.24e-34	Length:	575
Score:	532.00	Matches:	103
Percent Similarity:	69.23%	Conservative:	32
Best Local Similarity:	52.82%	Mismatches:	52
Query Match:	22.55%	Indels:	8
DB:	3	Gaps:	2

US-09-807-459-2 (1-458) x AF014758 (1-575)

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Db 14 GCAGAGGTGGTGGAGATGTGTCACCAAGCTTGCGAAGCAATGAGTTGTCATGCT 73
Oy 24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
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Db 74 GAAATGGAAGCAACTGAGCTCAACAAGATATGCAAAAGTCAATGCTATGTTAAGGAG 133
Oy 44 AsnPhaAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
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Db 134 ACCATTGTTGGTGGAGTGTGCGAAGAAAGTTGCTGGAATCTTCACTGCGGTGAGACGTA 193
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Db 194 ATTGCTATGTTAAACGCTGTGATGAGGCGATGTCGACGCTTGACAGCATG----- 247
Oy 84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAlaAla 103
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Db 248 -----AAGTACCAAGCCGTTGAGTGTGCAAAATCCTTACAGTTGGACGCTGCC 295
Oy 104 PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrp 123
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Db 296 TTCATGCTTTTACGGAAGATATTTCAACCTGCGAAGAAAGAGGTGAAGCGCTTCTCG 355
Oy 124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeu 143
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Db 356 ATGCGTTTCAGG-----AGCAGCCACGCGACCTACCATCTTGTGTTAGCTGTGG 409
Oy 144 GluLysAsnValThrArgSpAlaAspAlaThrAspIleGluAsnPheAlaSerAlaGlyTyr 163
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Db 410 AAGAAAGAAATGTTGTACGCAACCTGATATCAATGATGTTGAAGAAATTCGATCGCAGTAC 469
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Oy 164 LeuTyrMetAlaThrLeuLysTyrThrLysThrValAsnValAspLupheGlyAlaSer 183
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Db 470 TTCTACATACACTACGTTGACTACCAAGACTTACCTGACCTTACCTGAGCGGCGCTAAG 529
Oy 184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrPcLy 198
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Db 530 TTCTTACACAGCTTCTTCAACACTCCGCTGTGCGTTGCTTGGCT 574
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RESULT 32

AF014760

LOCUS Babesia bigemina S1A rap-1 alpha (rap-1) gene, partial cds. 575 bp DNA linear INV 31-JAN-2001

DEFINITION Babesia bigemina S1A rap-1 alpha (rap-1) gene, partial cds.

ACCESSION AF014760

VERSION AF014760.1 GI:2429261

KEYWORDS

SOURCE Babesia bigemina.

ORGANISM Babesia bigemina
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;

REFERENCE 1 (bases 1 to 575)

AUTHORS Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.

TITLE Genetic variation in the dimorphic regions of RAP-1 genes and rap-1

loci of *Babesia bigemina*

JOURNAL Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)

MEDLINE 98135662

AUTHORS Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-1997) Department of Veterinary Microbiology and

Pathology, Washington State University, Pullman, WA 99164-7040, USA

location/Qualifiers

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TLVYKTYLTVDFTAKFNFKLAFTRLFEGF"

BASE COUNT 145 a 119 c 153 g 158 t

ORIGIN

Alignment Scores:

Pred. No.:	1.24e-34	Length:	575
Score:	532.00	Matches:	103
Percent Similarity:	69.23%	Conservative:	32
Best Local Similarity:	52.82%	Mismatches:	52
Query Match:	22.55%	Indels:	8
DB:	3	Gaps:	2

US-09-807-459-2 (1-458) x AF014760 (1-575)

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Oy 4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
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Db 14 GCAGAGGTGGTGGAGATGTGTCACCAAGACTTCTGGAAGCAATGAGTTGTCATGCT 73
Oy 24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
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Db 74 GAAATGGAAGCAACTGAGCTCAACAAGATATGCAAAAGTCAATGCTATGTTAAGGAG 133
Oy 44 AsnPhaAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
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Db 134 ACCATTGTTGGTGGAGTGTGCGAAGAAAGTTGCTGGAATCTTCACTGCGGTGAGACGTA 193
Oy 64 SerAlaTyrMetSerArgCysAlaIleAspCysLeuThrLeuGlnSerLeuLysTyr 83
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Dn	194 ::: :::	
Oy	84	ProleugluAAlaLysTyrGlnProLeuthrLeupProAspProTyrGlnLeuGluaLa 103	
Dn	248	-----AACTACAAGCGCTGTGAGTCGCCAAATCCCTTACCACTGGACGCTGC 295	
Oy	104	PheIleLeuPheLysGLUserASpAlaSnProAlaSnSerThcLulsArghetrp 123	
Dn	296	TTCATGCTTTTCAGGAAGAAGTGATCTTAACCCTGGGAAGAAGAGTAGAGGCTTCGG 355	
Oy	124	MetArgPheArgARGLYLysasnHisSerTyrPheHISApLeuValPheasnLeu 143	
Dn	356	ATGCGTTGAGC-----AGCACCCACGCGCATACCTACTTGTGTTAGCTTGTG 409	
Oy	144	GluTysAsnValThrArgASpAlaSnAlaThrAspILegLusnPhelaSeraTyr 163	
Dn	410	AAGAAGATGTGTACGCGGACCCCTAATCCAATGATGTGAGAAGCTTGCATCGCAGTAC 469	
Oy	164	LeuTyrMeLalathLeuTyrTyrlusThryTrhrasnaValAspGluPheGlyAlaser 183	
Dn	470	TTCCTACAGACACTCTTGTACTACAAAGACTTACCAGCCGTGTGACTTTACGGCGGCTAAG 529	
Oy	184	PhePheAsnLysLeuSerPheThrChelyLeupPheGlyTPrgly 198	
Dn	530	TTCCTCAACAAGCTTGTCTTCAACAAGCTGCGCTGTGGTTCGGT 574	
RESULT 33			
LOCUS	AF014762	575 bp DNA linear INV 31-JAN-2001	
DEFINITION	Babesia bigemina uva rap-1 alpha (rap-1) gene, partial cds.		
ACCESSION	AF014762		
VERSION	AF014762.1 GI:2429265		
KEYWORDS	.		
SOURCE	Babesia bigemina.		
ORGANISM	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;		
REFERENCE	1 (bases 1 to 575)		
AUTHORS	Hotzel,I., Suarez,C.E., MCELwain,T.F. and Palmer,G.H.		
TITLE	Genetic variation in the dimorphic regions of RAP-1 genes and rap-1		
JOURNAL	lost of Babesia bigemina		
MEDLINE	Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)		
REFERENCE	2 (bases 1 to 575)		
AUTHORS	Hotzel,I., Suarez,C.E., MCELwain,T.F. and Palmer,G.H.		
TITLE	Direct submission		
JOURNAL	Submitted (16-JUL-1997) Department of Veterinary Microbiology and		
FEATURES	Pathology, Washington State University, Pullman, WA 99164-7040, USA		
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BASE COUNT	145 a 119 c 153 g 158 t		
ORIGIN			
Alignment Scores:	1.24e-34 Length: 575		
Fred. No.:	532.00 Matches: 103		
Percent Similarity:	69.23% Conservative: 32		

Query Match:	22.55%	Mismatches: 52	Indels: 8	Gaps: 2
US-09-807-459-2 (1-458) x AF014762 (1-575)				
QY 4	SerAspSerValGlyAspValThrIysThrLeuLeuAlaSerGluSerValAspSer 23			
DB 14	GGAGGAGGTGGTGGAGATGTGTCAAGACCTTGTGGGAAGCCAAATGAGCTGTCAATCT 73			
QY 24	AlaAlaAsnAlaTyrMetIleasnSerAspTyrLeuSerAlaValSerAsp 43			
DB 74	GAAATGGAAGCAACACAGCTGCAACAAGATATGCAAACTGATTTCTTAATGTTAAGAG 133			
QY 44	AsnPhaIaGluAlaArgIleCysSerGlnValProIysGlySerAsnCysSerAlaSerVal 63			
DB 134	ACCAATGTTGGTGGAGAGTGTGAGAAAGTTCGTGGAAACTCTACCTGGCGTGACAGCGTA 193			
QY 64	SerAlaTyrMetSerArgCysAlaIysGlnAspCysLeuThrLeuGlnSerLeuIysTyr 83			
DB 194	ATTGGCTTATGTTAAACCGTTGTGATGAGGCGCATTTGTCTGACGCTTGACACGATG- 247			
QY 84	ProLeuGluAlaIleTyrGlnProLeuThrLeuProAspProTyrGlnLeuGlnAla 103			
DB 248	-----AACTACAGAGCCGTGGAGTGTGACCTGCGCAATTCCTTACCAGTTGGAGCCTGCC 295			
QY 104	PhaIleuPhaIysGluSerAspAlaAsnProAlaAsnSerThrGluIysArgPheTrp 123			
DB 296	TCATGCTTTCATGAGGAAAGTATTTCTAACCTCGGAAAGAAAGAGTGAAGCGCTTTCGG 355			
QY 124	MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheasnLeuLeu 143			
DB 356	ATGCGCTTGAGG- - - - -AGCAGCCAGCGCGCATCATCTTTGTTGAGCTTGTG 409			
QY 144	GluIysAsnValThrArgAspAlaSerAlaThrAspIleGluAsnPhaIaSerArgTyr 163			
DB 410	AAGAAAGATGTTGTCACGCGACCCCTGAATCCAATGATGTTGGAGAACTTGCATCGAGTAC 469			
QY 164	LeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSer 183			
DB 470	TTCTACATGACACGCTTGTGACTACAAAGACTTACCGACCGTTGACTTTACGGCGGCTAAG 529			
QY 184	PhePheasnLysLeuSerPheThrThrClyLeuPheGlyTTPGly 198			
DB 530	TTCTTCAACAGAGCTTGTTCACACTGCGCGTTCGGTTCGGT 574			
RESULT 34				
AF014768				
LOCUS	AF014768	575 bp	DNA	linear
DEFINITION	Babesia bigemina UVA rap-1 beta (rap-1) gene, partial cds.			INV 31-JAN-2001
ACCESSION	AF014768			
VERSION	AF014768.1	GI:2429277		
KEYWORDS				
SOURCE	Babesia bigemina.			
ORGANISM	Babesia bigemina			
REFERENCE	1. (bases 1 to 575)			
AUTHORS	Hotzel,I.I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.			
TITLE	Genetic variation in the dimorphic regions of RAP-1 genes and rap-1			
JOURNAL	Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)			
MEDLINE	98135662			
REFERENCE	2. (bases 1 to 575)			
AUTHORS	Hotzel,I.I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.			
TITLE	Direct Submission			
JOURNAL	Submitted (15-JUL-1997) Department of Veterinary Microbiology and			
FEATURES	Pathology, Washington State University, Pullman, WA 99164-7040. USA			
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BASE COUNT 145 a 119 c 153 g 158 t

ORIGIN

Alignment Scores:
Pred. No.: 1.24e-34 Length: 575
Score: 532.00 Matches: 103
Percent Similarity: 69.23% Conservative: 32
Best Local Similarity: 52.82% Mismatches: 52
Query Match: 22.55% Indels: 8
DB: Gaps: 2

US-09-807-459-2 (1-458) x AF014768 (1-575)

OY 4 SeraspserValGlyAspValThrIleuLeuAlaIleSerGluSerValaspSer 23
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OY 24 AlaAlaAsnAlaIleuLeuLeuSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
DB 74 GAAATGGAAGCAACGTCAGTCAACAAGATGCAAGATGCAATGCTATGTTAAGAG 133
OY 44 AsnPhaIleuAlaIleuLeuSerGluValProIleuGlySerAsnGlySerAlaSerVal 63
DB 134 ACCATTGTTGGTGGAGTCTGCGAGAAAGTTCGTAACCTGCGCGGTGAGACGCTGA 193
OY 64 SerAlaIleuMetSerArgGlyAlaIleuGlySerGluSerLeuIleuSerLeuIleuSer 83
DB 194 ATTGGCTATGTTAACCGTGTGTATGAGGCGCATTTGTCTACGCTTGACGATG----- 247
OY 84 ProIleuGluAlaIleuLeuIleuProIleuLeuProIleuSerGluIleuGluAlaIleu 103
DB 248 -----AGTACCAAGCCGTTGAGTGTCCAAATGCTTACCAAGTTGGACGCTGCC 295
OY 104 PheIleuLeuPheIleuSerGluSerAlaAsnProIleuAlaAsnSerThrGluIleuSerPhe 123
DB 296 TTCATGCTTTTACGAGGAAGTATCTTACCTCGCAAGAAATGAGGTGAAAGCGCTTCTGG 355
OY 124 MetArgPheArgArgGlyIleuSerAsnIleuSerTyrPheIleuAspLeuValPheAsnLeu 143
DB 356 ATGCGTTCGAGG-----AGCAGCCACGCGGACCTACCACTCTTGTGTACCTGTGG 409
OY 144 GluIleuAsnValThrArgAspAlaAsnAlaSerAlaIleuAsnPheAlaSerArgTyr 163
DB 410 AAGAAAGATGTTGTATGCGACGATCCATGATGATGATGATGATGATGATGATGATGATG 469
OY 164 LeuTyrMetAlaIleuLeuTyrIleuTyrIleuThrIleuAsnValAspLeuPheGluAla 183
DB 470 TTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 529
OY 184 PhePheAsnIleuSerPheThrIleuPheGluIleuIleuIleuIleuIleuIleuIleu 198
DB 530 TTCCTACCAAGCTGTGCTTACCAACTGCGCTGTGCTGTGCTGTGCTGTGCTGTGCT 574

RESULT 35
AF014761 575 bp DNA linear INV 31-JAN-2001
LOCUS Babesia bigemina S2P rap-1 alpha (rap-1) gene, partial cds.
DEFINITION
ACCESSION AF014761
VERSION AF014761.1 GI:2429263
KEYWORDS
SOURCE Babesia bigemina.

ORGANISM Babesia bigemina
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Babesia.
REFERENCE 1 (bases 1 to 575)
AUTHORS Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
loci of Babesia bigemina
JOURNAL Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
MEDLINE 98135662
REFERENCE 2 (bases 1 to 575)
AUTHORS Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1997) Department of Veterinary Microbiology and
Pathology, Washington State University, Pullman, WA 99164-7040, USA

FEATURES
source
1..575
/organism="Babesia bigemina"
/strain="S2P"
/db_xref="taxon:5866"
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<1..>575
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/protein_id="AAC47863.2"
/translation="GVMSAEVYGVDSKTLLEANEVNAEMETOVNKKMOSLSNVKE
TIVGECKEVAGNSTCGESVIAVYVRCDEGCLTDSMKYKPLSPNPYOLDAAFMFL
RESDSNPAKNEVKRPMRMSRSHGDIHFVYVSLKKNVVRDPSNDVENFASQYFYMT
TLVYKTYLVDTFAKFNKLAFTTRFLGFG"

BASE COUNT 145 a 119 c 152 g 159 t

ORIGIN

Alignment Scores:
Pred. No.: 3.14e-34 Length: 575
Score: 527.00 Matches: 102
Percent Similarity: 69.11% Conservative: 30
Best Local Similarity: 53.40% Mismatches: 51
Query Match: 22.34% Indels: 8
DB: Gaps: 2

US-09-807-459-2 (1-458) x AF014761 (1-575)

OY 8 GlyAspValThrIleuLeuLeuAlaIleSerGluSerValaspSerAlaIleAla 27
DB 26 GGAGATGTGTCCAGACCTTGCTGGAAGCCAAATGAGTTGCTGAATGAGAGCA 85
OY 28 TyrMetIleuSerAspMetSerAspTyrLeuSerAlaValSerAspAsnPhaIleu 47
DB 86 ACTGACGTCACAAATATGCAAAAGTCTTCTATGTTAAGGAGACCATTTGCTGGT 145
OY 48 ArgIleCysSerGluValProIleuGlySerAsnGlySerAlaSerValSerAlaTyrMet 67
DB 146 GAGTGTGCGAGAAAGTGTGGAACCTGCTACCTGCGGTGAGAGCGTAATGCTATGTT 205
OY 68 SerArgCysAlaIleuSerGluSerLeuIleuSerLeuIleuSerLeuIleuSerLeu 87
DB 206 AACCGTTGATGATGAGGCGCATTTGTCAGCCTTGACAGCATG----- 247
OY 88 LysTyrGluProIleuThrIleuProAspProTyrGluLeuGluAlaIlePheIleuPhe 107
DB 248 AAGTACAGCCGTTGAGTGTGCAAAATCTTACCAATGAGACCTGCTTACGCTTTTC 307
OY 108 LysGluSerAspAlaAsnProIleuAsnSerThrGluIleuArgPheThrPheArgPhe 127
DB 308 AGGAAAGATGATCTTAACCTCGGAAGATGAGGTGAGAGCGCTTGATGATGATGATG 367
OY 128 ArgGlyIleuAsnIleuSerTyrPheIleuIleuValPheAsnLeuLeuGluIleuAsnVal 147
DB 368 -----AGCAGCCACGCGACATCACTCACTTGTGTTGTTGTTGTTGTTGTTGTT 421
OY 148 ThrArgAspAlaSerAlaIleuThrIleuGluAsnPheAlaSerArgTyrIleuTyrMetAla 167

QY	168	ThrLeuTyrTyrTyrTyrTyrThrAsnValAspGluPheGlyAlaSerPheAsnIys	187
Db	482	ACGTTGCTACTACAAAGACTTACCTGACCGCTTGACCTTACGCGGCTAAAGTCTTCAACAAG	541
QY	188	LeuSerPheThrThrGlyLeuPheGlyTyrPglY	198
Db	542	CTTGCTTTCACAACTCGCCTGTCGTTTCGCT	574
RESULT 36	AF014767	575 bp	DNA linear INV 31-JAN-2001
LOCUS	Babesia bigemina S2P rap-1 beta (rap-1) gene, partial cds.		
DEFINITION	AF014767		
ACCESSION	AF014767.1	GI:2429275	
VERSION			
KEYWORDS			
SOURCE	Babesia bigemina.		
ORGANISM	Babesia bigemina		
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.		
AUTHORS	Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.		
TITLE	Genetic variation in the dimorphic regions of rap-1 genes and rap-1 loci of Babesia bigemina		
JOURNAL	Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)		
MEDLINE	98135662		
REFERENCE	2 (bases 1 to 575)		
AUTHORS	Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUL-1997) Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164-7040, USA		
FEATURES	Location/Qualifiers		
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	/protein_id="AAC47869.2"		
	/db_xref="GI:12622036"		
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	RESQNPAPKNENKRFPMKRSRSHGDYHFFVYSLLKKNVRDPESDVENFASQYFYWT		
	TLVYKTLTVDTFAKFFNKLAFTTRIFGCG"		
BASE COUNT	145 a 119 c 152 g 159 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	3,14e-34	Length:	575
Score:	527.00	Matches:	102
Percent Similarity:	69.11%	Conservative:	30
Best Local Similarity:	53.40%	Mismatches:	51
Query Match:	22.34%	Indels:	8
DB:	3	Gaps:	2
US-09-807-459-2 (1-458) x AF014767 (1-575)			
QY	8	GI:AAAPVALThbLysThrLeuLeuLalLalSerGluSerValASPSeRAlAlaLalasnAla	27
Db	26	GGAGATGTGTCCAAAGACCTTGCTGGAAACCAATGAGGTTGTCATAGCTGGAATGAGAACCA	85
QY	28	TyrMetLiasnSerAspMetSerAspTyrLeuSerAlaValASerAspAsnPhaLaGlu	47
Db	86	ACTCAGTCGCAACGAATATGCAAGTCATATGCTAATGTAAAGAGACCATTTGCT	145
QY	48	ArgLieCysSerGlnValProLysGlySerAsnCysSerAlaSerAlaTyrMet	67

Db	Accession	Gene	Protein	Length	Score	E-value
Db	146	GAGGGTCGGAGAAAGTTGCTGGAAACCTTACCTCGGGGAGACGGTAATTCCATGTT		205		
Qy	68	SerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyrProLeuGlnAla	87			
Db	206	MAACCTTGGATAGAGGGCGATGCTGTGACCGTTGACGATG-----	247			
Qy	88	LysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGlnAlaAlaPheIleLeuPhe	107			
Db	248	AGGTACAAACCGCTTAGTGTGCGCAATCTCTTACAGTTGGAGCGTGCCTTACGCTTTC	307			
Qy	108	LysGlnSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrpMetArgPheArg	127			
Db	308	ACGGAAAGATGATTCAACCCCTGCAAGATGAGTGGAAGCCGCTTGTGGATGCGTTCGAGG	367			
Qy	128	ArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeuGlnLysAsnVal	147			
Db	368	-----ACGAGCCAGCGGCGACCTACCATCTTGTGTGTTAGCTTTTGAGAGAGATGTT	421			
Qy	148	ThrArgAspAlaAspAlaThrAspIleGlnAsnPheAlaSerArgTyrLeuTyrMetAla	167			
Db	422	GTACGGAGACCTTGAAATCCAAATGATGCTGTGAGACTTCGCATCTTACATGACT	481			
Qy	168	ThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSerPheAsnLys	187			
Db	482	ACGTTGTACTACAAACCTTACCTGACCGCTTGACTTTACGGCGGCTTAAGTCTTCAACAAG	541			
Qy	188	LeuSerPheThrThrGlyLeuPheGlyArgLys	198			
Db	542	CTTGCTTTCACAACTCGCCTGTTCGGTTTCGCT	574			
RESULT 37						
LOCUS	AF014764	574 bp	DNA	linear	INV 31-JAN-2001	
DEFINITION	Babesia bigemina CGP rap-1 beta (rap-1) gene, partial cds.					
ACCESSION	AF014764					
VERSION	AF014764.1 GI:2429269					
KEYWORDS						
SOURCE						
ORGANISM	Babesia bigemina. Babesia bigemina Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.					
REFERENCE	1 (bases 1 to 574) Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H. Genetic variation in the dimorphic regions of RAP-1 genes and rap-1 loci of Babesia bigemina Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)					
JOURNAL	2 (bases 1 to 574) Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H. Direct Submission Submitted (16-JUL-1997) Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164-7040, USA					
FEATURES	Location/Qualifiers 1..574 /organism="Babesia bigemina" /strain="CGP" /db_xref="taxon:5866" <1..>574 /gene="rap-1" <1..>574 /gene="rap-1" /codon_start=1 /product="rap-1 beta" /protein_id="AAC47866.2" /db_xref="GI:12622033" /translation="GCTYSRVGCVSTLLAANEVNAEMEAQINDMKTIOLANKE TIVDEVCRKADGSPTRKRSVLAIVDRDEGCLTLDMSKTKIPVLPVLODAFMLE RESQSNPAKNKNGVRFPMKSRSHGDYHFFVSLTKKNVRDPESDNDEVNARSQFYVMT TLVYKTLTVDFTAAKFFNKLAFTTRIFGCG"					
BASE COUNT	142 a 124 c 156 g 152 t					
ORIGIN						

Pred. No.: 1,15e-33 Length: 574
 Score: 520.00 Matches: 102
 Percent Similarity: 68.75% Conservative: 30
 Best Local Similarity: 53.12% Mismatches: 52
 Query Match: 22.04% Indels: 8
 DB: 3 Gaps: 2

US-09-807-459-2 (1-458) x AF014764 (1-574)

OY 7 ValGlyaspValThrLysThrLeuLeuAlaAlaSerGluSerValAlaSerAlaAlaAsn 26
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 DB 22 GTTGAGAGATGTGTCCAGACCTTGCTGGCAGCAAGACGATGTCATGCAATGCAATGCA 81
 OY 27 AlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAspAsnPha 46
 |||||
 DB 82 GCAGCTCAGATTACGAAAGATATGAAATTCAGTTGGCGACCTGACAGGACCATCGTT 141
 OY 47 GluATGilecySerGlnValProLysGlySerAsnCySerAlaSerAlaSerAlaTyr 66
 |||||
 DB 142 GATGAGGTCTCGAAGAAAGATGCTGGAACCCCTACGTGCGCGAAGACGCTAATGCTTAT 201
 OY 67 MetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyrProLeuGlu 86
 |||||
 DB 202 GTTGACCGTTGTGATGAGCGCGATGCTGTGACGCTTGACACGATG----- 246
 OY 87 AlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGlnAlaAlaPheIleLeu 106
 |||||
 DB 247 ---AAGTACAAAGCCGTGTGCTGCTGCTTAATCCATGACCTGACCTTCATGCTT 303
 OY 107 PheLysGluSerAspAlaAsnProAlaAsnSerThrGlnLysArgPheThrPheTargPhe 126
 |||||
 DB 304 TTCAGAGAAAGATGATTCATACCTCGAAGATGAGGTAAACCCCTTCGATGCTTGG 363
 OY 127 ArgAArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeuLysAsn 146
 |||||
 DB 364 AGG-----AGCAGCCACGCGACCTACCATCTTGTGTGTTGATGCTTGAAGAAGAT 417
 OY 147 ValThrArgAspAlaAsnProAlaAsnSerThrGlnLysArgPheThrPheTargPhe 166
 |||||
 DB 418 GTTGACGCGACCTGAAATGCAATGATGTTGAGAACTGCGATCGATCTTCAATG 477
 OY 167 AlaThrLeuTyrTyrLysThrTyrThrAsnValAlaAspGlyAlaSerPhePheAsn 186
 |||||
 DB 478 ACTAGCTGTACTACAGACTTACCTGACCGCTTGACTTACGCGGCTAAGTTCTTCAAC 537
 OY 187 LysLeuSerPheThrThrGlyLeuPheGlyTyrGly 198
 |||||
 DB 538 AAGCTTGCTTCCACAACCTCGCTGCTGCTGCTGCT 573
 RESULT 38
 LOCUS AF014759 823 bp DNA linear INV 31-JAN-2001
 DEFINITION Babesia bigemina PTR rap-1 alpha (rap-1) gene, partial cds.
 ACCESSION AF014759
 VERSION AF014759.1 GI:2429259
 KEYWORDS
 SOURCE
 ORGANISM
 Babesia bigemina.
 Babesia bigemina
 Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
 Babesia.
 1 (bases 1 to 823)
 Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
 Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
 loci of Babesia bigemina
 Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
 MEDLINE
 JOURNAL 98135662
 REFERENCE
 AUTHORS 2 (bases 1 to 823)
 Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
 Direct Submission
 JOURNAL Submitted (16-JUL-1997) Department of Veterinary Microbiology and
 Pathology, Washington State University, Pullman, WA 99164-7040, USA
 FEATURES
 source
 1..823 Location/Qualifiers

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 /db_xref="taxon:5866"
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 G"

BASE COUNT 202 a 173 c 208 g 240 t
 ORIGIN

Alignment Scores:

Pred. No.: 1.78e-33 Length: 823
 Score: 520.00 Matches: 101
 Percent Similarity: 68.72% Conservative: 33
 Best Local Similarity: 51.79% Mismatches: 53
 Query Match: 22.04% Indels: 8
 DB: 3 Gaps: 2

US-09-807-459-2 (1-458) x AF014759 (1-823)

OY 4 SerAspSerValGlyaspValThrLysThrLeuLeuAlaSerGluSerValAspSer 23
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 DB 262 GCAGAGCTGTGTGAGATGTGTCCAGACCTTGCTGGAACCATGATGCTGATGCTAT 321
 OY 24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
 |||||
 DB 322 GAATGGAAGCAACATGAGTCAACAAGATATGCAAAAGTCAATGTCTAATGTTAAGAG 381
 OY 44 AsnPhaLagLuarGlyLeuSerGlnValProLysGlySerAsnCySerAlaSerAla 63
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 DB 382 ACCATCGTTGATGAGGTGTGCGAAGAAAGATGCTGAACCTTACCTGCGGTGAGACGTA 441
 OY 64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
 |||||
 DB 442 ATTGCTATGTTACCGTGTGTATGAGGCGGATGTGTGACGCTTGACACGATG----- 495
 OY 84 ProLeuGlnAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGlnAlaAla 103
 |||||
 DB 496 -----AAGTACAAAGCCGTGAGCTGCTCCAAATCCTTACACGATTGCGACGCTGCC 543
 OY 104 PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGlnLysArgPheTargPhe 123
 |||||
 DB 544 TTCATGCTTTTTCAGGAAAGATGTTCTTAACCCGCAAGATGAGTGAAGTGCCTTCTGG 603
 OY 124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeu 143
 |||||
 DB 604 ATGCGTTCCAGG-----AGCAGCCACGCGGACTACCACTTCTTGTGTACTTGTG 657
 OY 144 GluLysAsnValThrArgAspAlaAsnProAlaAsnSerThrGlnLysArgPheTargPhe 163
 |||||
 DB 658 AAGAAAGATGTGTGACGCGACCTGAATCCAAATGATGTTGAGAACTCGCATCGCAGTAC 717
 OY 164 LeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAlaAspLupheGlyAlaSer 183
 |||||
 DB 718 TTCTACATGACTACGTTGTTGTTACCAAGATGATGTTACCTGACCGCTTACCGCGCTAAG 777
 OY 184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrGly 198
 |||||
 DB 778 TTCTTACCAAGCTTCTTACCACTCGCGCTGTGCTTGGCTTGGCT 822
 RESULT 39
 LOCUS AF014763 575 bp DNA linear INV 31-JAN-2001
 DEFINITION Babesia bigemina CGA rap-1 alpha (rap-1) gene, partial cds.

ACCESSION AF014763 GI:2429267
 VERSION AF014763.1
 KEYWORDS
 SOURCE Babesia bigemina.
 ORGANISM Babesia bigemina; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.

REFERENCE 1 (bases 1 to 575)
 Hotzel, I., Suarez, C.E., McElwain, T.F. and Palmer, G.H.
 Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
 TITLE loci of Babesia bigemina
 JOURNAL Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
 MEDLINE 98135662
 REFERENCE 2 (bases 1 to 575)
 Hotzel, I., Suarez, C.E., McElwain, T.F. and Palmer, G.H.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-1997) Department of Veterinary Microbiology and
 Pathology, Washington State University, Pullman, WA 99164-7040, USA
 FEATURES
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BASE COUNT 144 a 123 c 156 g 152 t

ORIGIN

Alignment Scores:
 Pred. No.: 4,25e-33 Length: 575
 Score: 513.00 Matches: 101
 Percent Similarity: 68.21% Conservative: 32
 Best Local Similarity: 51.79% Mismatches: 54
 Query Match: 21.75% Indels: 8
 DB: 3 Gaps: 2

US-09-807-459-2 (1-458) x AF014763 (1-575)

QY 4 SeraspserValIGlyAspValThrlYsrThrlLeuLeuAlaAlaSerGluSerValAspSer 23
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 DB 14 GCAGAGGTGTGGAGATGTCACAGACCTTGCCTGCAGCCAGAGGTTGTCATGCT 73
 : : : : :
 QY 24 AlaAlaAnaLatYrMetIleAsnSerAspMetSerAspYrLeuSerAlaValSerAsp 43
 : : : : :
 DB 74 GAATGGAAGACGTCAGATTAACGAGATATGAAGATTCACTTGGCCAGACGTCAAGAG 133
 : : : : :
 QY 44 AsnPhelaGluArgIleCysSerGlnValIProLysGlySerAsnGlySerAlaSerVal 63
 : : : : :
 DB 134 ACCATCGTGTGATGAGTGTGCAGAAACATGCTGGAACCTCTACCTGCCGCAAGAGCTTA 193
 : : : : :
 QY 64 SerAlaYrMetSerArgCysAlaLysGlnAspGlyLeuThrlLeuGlnSerLeuLysTyr 83
 : : : : :
 DB 194 AWTCCCTATGTGTGACCGTGTGATGAGCGGATGCTGTGACGCTTGACAGCATG---- 247
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 QY 84 ProLeuGluAlaLysTyrGlnProLeuThrlLeuProAspProTyrGlnLeuGluAlaAla 103
 : : : : :
 DB 248 -----AACTACAGACCGTGTGAGTGTGCCAAATCTTTCACCACTTGGAGCGTCC 295
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 QY 104 PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrlGluLysArgPheTyr 123
 : : : : :
 DB 296 TTTCATGCTTTTCAGGAAGATGATTAACCTTCGGAAGATGAGGTCAAGTCTTCTGCG 355
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 QY 124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeu 143

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 DB 356 ATGCGTTCAGAG-----AGCAGCCAGCGCAGTACCATCTTGTGTGATGCTGTG 409
 : : : : :
 QY 144 GluLysAsnValThrlArgAspAlaAspAlaThrAspIleGluAsnPhaAlaSerArgTyr 163
 : : : : :
 DB 410 AAGAAGATGTGTGACCGGACCTGCAATCATATGTTGAGAACTTCGATCCGACATAC 469
 : : : : :
 QY 164 LeuYrMetAlaThrlLeuTyrTyrThrlYsrThrlAsnValAspGluPhGlyAlaSer 183
 : : : : :
 DB 470 TTTCATGACTACTGCTTACTACTACAGACTTACCGCTTGAACCTTACCGCGCTAG 529
 : : : : :
 QY 184 PhePheAsnLysLeuSerPheThrlThrlGlyLeuPheGlyTyrGly 198
 : : : : :
 DB 530 TTCTTCACACAGCTGCTTTCACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
 : : : : :
 RESULT 40
 AF014765 866 bp DNA linear INV 31-JAN-2001
 LOCUS
 DEFINITION Babesia bigemina ppr rap-1 beta (rap-1) gene, partial cds.
 ACCESSION AF014765
 VERSION AF014765.1 GI:2429271
 KEYWORDS
 SOURCE Babesia bigemina.
 ORGANISM Babesia bigemina; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.

REFERENCE 1 (bases 1 to 866)
 Hotzel, I., Suarez, C.E., McElwain, T.F. and Palmer, G.H.
 Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
 TITLE loci of Babesia bigemina
 JOURNAL Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
 MEDLINE 98135662
 REFERENCE 2 (bases 1 to 866)
 Hotzel, I., Suarez, C.E., McElwain, T.F. and Palmer, G.H.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-1997) Department of Veterinary Microbiology and
 Pathology, Washington State University, Pullman, WA 99164-7040, USA
 FEATURES
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 G"

BASE COUNT 208 a 184 c 227 g 247 t

ORIGIN

Alignment Scores:
 Pred. No.: 6,98e-33 Length: 866
 Score: 513.00 Matches: 101
 Percent Similarity: 68.21% Conservative: 32
 Best Local Similarity: 51.79% Mismatches: 54
 Query Match: 21.75% Indels: 8
 DB: 3 Gaps: 2

US-09-807-459-2 (1-458) x AF014765 (1-866)

QY 4 SeraspserValIGlyAspValThrlYsrThrlLeuLeuAlaAlaSerGluSerValAspSer 23
 : : : : :
 DB 305 GCAGAGGTGTGGAGATGTCACAGACCTTGCCTGCAGCCAGAGGTTGTCATGCT 364
 : : : : :
 QY 24 AlaAlaAnaLatYrMetIleAsnSerAspMetSerAspYrLeuSerAlaValSerAsp 43

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Db 365 GAAATGAGACGCTCAGATTACGAGATTAAGATTACACTGGCGAACSTCAAGAG 424
Oy 44 AsnPhelaIaGluArgIleCysSerGlnValProIylsGlySerAsnCysSerAlaSerVal 63
Db 425 ACCATCGTTGAGTGCAGAAAGATGCTGGAAGCCCTACCTGCGCAAGAGCGTA 484
Oy 64 SerAlaTyrMetSerArgCysAlaIylsGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
Db 485 ATGCGCTTATGTCAGCGTTGTGATGAGGCGCATTTGTGACGCTTGACAGCATG----- 538
Oy 84 ProLeuGluAlaIylsTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAlaIa 103
Db 539 -----AAGTACAGCGCGTTGAGTGCAGCAATCCCTTACAGTTGAGCGCTGCC 586
Oy 104 PheIleLeuPheIylsGluSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrp 123
Db 587 TTCATGCTTTTCAGGGAAGTCAATCTTAACCTCGCAAGAAATGAGGTGAAGTCTTCTGG 646
Oy 124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeu 143
Db 647 ATGCGTTCGAGG-----AGCAGCCACGCGCGACTACATCCTTGTGTGTTAGCTTGTG 700
Oy 144 GluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr 163
Db 701 AAGAGATGTTGTGACGCGAGCCCTGATCCATGATGTTGAGAACTTCGCATCGCAGTAC 760
Oy 164 LeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSer 183
Db 761 TTCCTACATGACTGCTGTACTACAAAGACTTACCTGACCGCTTACGCGGCGCTAAG 820
Oy 184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrPgly 198
Db 821 TTCCTCAACAAGCTTGTTCACAACTCGCCCTGTTCGGTTTCGGT 865
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Job time : 1978 secs

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